



13

SEQUENCE LISTING

- <110> Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350
<141> 2000-09-18
- <150> PCT/US00/04414
<151> 2000-02-22
- <150> US 60/143,048
<151> 1999-07-07
- <150> US 60/145,698
<151> 1999-07-26
- <150> US 60/146,222
<151> 1999-07-28
- <150> PCT/US99/20594
<151> 1999-09-08
- <150> PCT/US99/20944
<151> 1999-09-13
- <150> PCT/US99/21090
<151> 1999-09-15

<150> PCT/US99/21547
<151> 1999-09-15

<150> PCT/US99/23089
<151> 1999-10-05

<150> PCT/US99/28214
<151> 1999-11-29

<150> PCT/US99/28313
<151> 1999-11-30

<150> PCT/US99/28564
<151> 1999-12-02

<150> PCT/US99/28565
<151> 1999-12-02

<150> PCT/US99/30095
<151> 1999-12-16

<150> PCT/US99/30911
<151> 1999-12-20

<150> PCT/US99/30999
<151> 1999-12-20
<150> PCT/US00/00219
<151> 2000-01-05

<160> 423

<210> 1
<211> 1825
<212> DNA
<213> Homo sapiens

<400> 1
actgcacctc ggttctatcg attgaattcc cgggggatcc tctagagatc cctcgacctc 60
gacccacgcg tccggggcccg agcagcacgg cgcaggacc tggagctccg gctgcgtctt 120
cccgacgcgc taccgcccat gcgcctgccg cgcggggccg cgctggggct cctgccgctt 180
ctgctgctgc tgcgcgccgc gccggaggcc gccaaagaagc cgacgccctg ccaccggtgc 240
cgggggctgg tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300
ggcggaaca cggcttgga ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360
ctgctggaga tcctggaggg gctgtgcgag agcagcgact tcgaatgcaa tcagatgcta 420
gaggcgcagg aggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480
ttattcgagt ggttttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggt 540
cccactgtc tcgcatgcca gggcgatcc cagaggcctt gcagcgggaa tggccactgc 600
agcggagatg ggagcagaca gggcgacggg tcctgccggt gccacatggg gtaccagggc 660
ccgctgtgca ctgactgcat ggacggctac ttcagctcgc tccggaacga gaccacagc 720
atctgcacag cctgtgacga gtccctgcaag acgtgctcgg gcctgaccaa cagagactgc 780
ggcgagtgtg aagtgggctg ggtgctggac gagggcgctt gtgtggatgt ggacgagtgt 840
gcggccgagc cgcctccctg cagcgtgcg cagttctgta agaacgcaa cggctcctac 900
acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag gggaaggccc aggaaactgt 960
aaagagtgtg tctctggcta cgcgaggag caccggacagt gtgcagatgt ggacgagtgc 1020
tcactagcag aaaaaacctg tgtgaggaaa aacgaaaact gctacaatac tccagggagc 1080
tacgtctgtg tgtgtcctga cggcttcgaa gaaacggaag atgcctgtgt gccgccggca 1140

```

gaggctgaag ccacagaagg agaaagcccc acacagctgc cctcccgcga agacctgtaa 1200
tgtgccggac ttacccttta aattattcag aaggatgtcc cgtggaaaat gtggccctga 1260
ggatgccgtc tcctgcagtg gacagcggcg gggagaggct gcctgctctc taacggttga 1320
ttctcatttg tcccttaaag agctgcattt cttggttggt cttaaacaga cttgtatatt 1380
ttgatacagt tctttgtaat aaaattgacc attgtaggta atcaggagga aaaaaaaaaa 1440
aaaaaaaaaa aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1500
gcccacttg tttattgcag cttataatgg ttacaaataa agcaatagca tcacaaattt 1560
cacaaataaa gcattttttt cactgcattc tagttgtggt ttgtccaaac tcatcaatgt 1620
atcttatcat gtctggatcg ggaattaatt cggcgcagca ccatggcctg aaataacctc 1680
tgaaagagga acttggttag gtaccttctg aggcggaaag aaccagctgt ggaatgtgtg 1740
tcagttaggg tgtggaaagt ccccaggctc cccagcaggc agaagtatgc aagcatgcat 1800
ctcaattagt cagcaacca gtttt                                     1825

```

<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
  1              5              10              15

```

```

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
      20              25              30

```

```

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35              40              45

```

```

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50              55              60

```

```

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65              70              75              80

```

```

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
      85              90              95

```

```

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100             105             110

```

```

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115             120             125

```

```

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
      130             135             140

```

```

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
      145             150             155             160

```

```

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
      165             170             175

```

```

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
      180             185             190

```

```

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
      195             200             205

```

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
 210 215 220
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
 225 230 235 240
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
 245 250 255
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
 260 265 270
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
 275 280 285
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
 290 295 300
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
 305 310 315 320
 Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
 325 330 335
 Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
 340 345 350

Leu

<210> 3
 <211> 2206
 <212> DNA
 <213> Homo sapiens

<400> 3
 cagggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatcctc tagagatccc 60
 tgcacctcga cccacgcgtc cgccaggccg ggaggcgacg cgcccagccg tctaaacggg 120
 aacagccctg gctgaggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180
 ggtgcgccac gaggagtttt cccggcagcg aggaggtcct gagcagcatg gcccggagga 240
 gcgccttccc tgcgcgcg cgcttggtct ggagcatcct cctgtgcctg ctggcactgc 300
 gggcggaggc cgggcgcgcg caggaggaga gcctgtacct atggatcgat gctcaccagg 360
 caagagtact cataggattt gaagaagata tcctgattgt ttcagagggg aaaatggcac 420
 cttttacaca tgatttcaga aaagcgcaac agagaatgcc agctattcct gtcaatatcc 480
 attccatgaa ttttacctgg caagctgcag ggcaggcaga atacttctat gaattcctgt 540
 ccttgcgctc cctggataaa ggcacatgag cagatccaac cgtcaatgtc cctctgctgg 600
 gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtcct ggaaaacagg 660
 atgggggtggc agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccattc 720
 tccaaacacc tcaaatgct atcttcttta aaacatgtca acaagctgag tgcccaggcg 780
 ggtgcccgaat tggaggcttt tgtaatgaaa gacgcacatc cgagtgtcct gatgggttcc 840
 acggacctca ctgtgagaaa gccctttgtt ccccacgatg tatgaatggt ggactttgtg 900
 tgactcctgg tttctgcac tgcccacctg gattctatgg agtgaactgt gacaaagcaa 960
 actgctcaac cacctgcttt aatggaggga cctgtttcta ccctggaaaa tgtatttgcc 1020
 ctccaggact agaggagag cagtgtgaaa tcagcaaatg cccacaaccc tgtcgaaatg 1080
 gaggtaaatg cattggtaaa agcaaagtga agtggtccaa aggttaccag ggagacctct 1140
 gttcaaagcc tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaaccaaca 1200

```

aatgccaatg tcaagaaggt tggcatggaa gacactgcaa taaaaggtac gaagccagcc 1260
tcatacatgc cctgaggcca gcaggcgccc agctcaggca gcacacgcct tcacttaaaa 1320
aggccgagga gcggcgggat ccacctgaat ccaattacat ctggtgaact cgcacatctg 1380
aaacgtttta agttacacca agttcatagc ctttggttaac ctttcatgtg ttgaatgttc 1440
aaataatggt cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500
actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag catgatggta 1560
tagattttct tgtttcagtg ctttgggaca gattttatat tatgtcaatt gatcagggtta 1620
aaattttcag tgtgtagttg gcagatattt tcaaaattac aatgcattta tgggtgtctgg 1680
gggcagggga acatcagaaa ggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg 1740
atggtgcagt taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata tattttgacc 1860
ttaccattat tccagagatt cagtattaaa aaaaaaaaaa ttacactgtg gtagtggcat 1920
ttaacaata taatatattc taaacacaat gaaataggga atataatgta tgaacttttt 1980
gcattggcct gaagcaatat aatatattgt aaacaaaaca cagctcttac ctaataaaca 2040
ttttatactg tttgtatgta taaaataaag gtgctgcttt agtttttttg aaaaaaaaaa 2100
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgccgc gactctagag tcgacctgca 2160
gaagcttggc cgccatggcc caacttgttt attgcagctt ataatg 2206

```

<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
  1              5              10              15

```

```

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
      20              25              30

```

```

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
  35              40              45

```

```

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
  50              55              60

```

```

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
  65              70              75              80

```

```

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
      85              90              95

```

```

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
  100              105              110

```

```

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
  115              120              125

```

```

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
  130              135              140

```

```

Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
  145              150              155              160

```

```

Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
      165              170              175

```

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
 340 345 350
 Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
 355 360 365
 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 5

agggagcacg gacagtgtgc agatgtggac gattgctcac tagca

45

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 6
 agagtgtatc tctggctacg c 21

<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 7
 taagtccggc acattacagg tc 22

<210> 8
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 8
 cccacgatgt atgaatggtg gacttttgtgt gactcctggt ttctgcatc 49

<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 9
 aaagacgcat ctgcgagtgt cc 22

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 10
 tgctgatttc acactgctct ccc 23

<210> 11
 <211> 2197
 <212> DNA

<213> Homo sapiens

<400> 11

```
cgagcgcgtg ggcgtccggc ggtcgcagag ccaggaggcg gaggcgcgcg ggccagcctg 60
ggccccagcc cacaccttca ccaggggccca ggagccacca tgtggcgatg tccactgggg 120
ctactgctgt tgctgccgct ggctggccac ttggctcttg gtgccagca gggtcgtggg 180
cgccgggagc tagcaccggg tctgcacctg cggggcatcc gggacgcggg aggccggtac 240
tgccaggagc aggacctgtg ctgccgcggc cgtgccgacg actgtgccct gccctacctg 300
ggcgccatct gttactgtga cctcttctgc aaccgcacgg tctccgactg ctgccctgac 360
ttctgggact tctgcctcgg cgtgccaccc ccttttcccc cgatccaagg atgtatgcat 420
ggaggtcgta tctatccagt cttgggaacg tactgggaca actgtaaccg ttgcacctgc 480
caggagaaca ggcagtggca tgggtggatcc agacatgatc aaagccatca accagggcaa 540
ctatggctgg caggctggga accacagcgc cttctggggc atgaccctgg atgagggcat 600
tcgctaccgc ctgggcacca tccgcccac ttcctcggtc atgaacatgc atgaaattta 660
tacagtgtgt aacccagggg aggtgcttcc cacagccttc gaggcctctg agaagtggcc 720
caacctgatt catgagcctc ttgaccaagg caactgtgca ggctcctggg ccttctccac 780
agcagctgtg gcatccgatc gtgtctcaat ccattctctg ggacacatga cgcctgtcct 840
gtcgcgccag aacctgtgtt cttgtgacac ccaccagcag cagggtgccg gcggtgggcg 900
tctcgatggt gcctgggtgt tcttgctcgg ccgtgcggcg gtgtctgacc actgctacc 960
cttctcgggc cgtgaacgag acgaggctgg ccctgcggcc ccctgtatga tgcacagccg 1020
agccatgggt cggggcaagc gccaggccac tgcccactgc cccaacagct atgttaataa 1080
caatgacatc taccaggtca ctctgttcta ccgctcggc tccaacgaca aggagatcat 1140
gaaggagctg atggagaatg gccctgtcca agcctcatg gaggtgcatg aggacttctt 1200
cctatacaag ggaggcatct acagccacac gccagtgagc cttgggaggc cagagagata 1260
ccgccggcat gggacccact cagtcaagat cacaggatgg ggagaggaga cgctgccaga 1320
tggaaggacg ctcaaatact ggactgcggc caactcctgg ggcccagcct ggggagagag 1380
gggccacttc cgcctcgtgc gcggcgtcaa tgagtgcgac atcgagagct tcgtgctggg 1440
cgtctggggc cgctgaggca tggaggacat gggtcacac tgaggctgcg ggcaccacgc 1500
ggggtcgggc ctgggatcca ggctaagggc cggcggaaga ggcccaatg gggcggtgac 1560
cccagcctcg cccgacagag cccggggcgc aggcgggcgc caggcgcta atccgggcg 1620
gggttccgct gacgcagcgc cccgcctggg agccgcgggc aggcgagact ggcggagccc 1680
ccagacctcc cagtggggac ggggcagggc ctggcctggg aagagcacag ctgcagatcc 1740
caggcctctg gcgccccac tcaagactac caaagccagg acacctcaag tctccagccc 1800
caatacccca ccccaatccc gtattctttt tttttttttt ttagacaggg tcttgctccg 1860
ttgcccaggc tggagtgcag tggcccatca gggctcactg taacctccga ctctgggtt 1920
caagtgacct tcccacctca gcctctcaag tagctgggac tacaggtgca ccaccacacc 1980
tggctaattt ttgtattttt tgtaaagagg ggggtctcac tgtgttgccc aggtgtgtt 2040
cgaactcctg ggctcaagcg gtccacctgc ctccgcctcc caaagtgtg ggattgcagg 2100
catgagccac tgcaccacgc cctgtattct tattcttcag atatttattt ttcttttcac 2160
tgttttaaaa taaaaccaa gtattgataa aaaaaa 2197
```

<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

```
Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Pro Leu Ala Gly
  1                      5                      10                      15

His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
      20                      25                      30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35                      40                      45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
```


50	55	60
Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr		
65	70	75 80
Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro		
	85	90 95
Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr		
	100	105 110
Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln		
	115	120 125
Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln		
	130	135 140
Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly		
145	150	155 160

His Asp Pro Gly

<210> 13
 <211> 533
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (33)..(33)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (37)..(37)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (80)..(80)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (94)..(94)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (144)..(144)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (188)..(188)
 <223> a, t, c or g

<400> 13
aggctccttg gccctttttc cacagcaagc ttntgcnatc ccgattcgtt gtctcaaate 60
caattctctt gggacacatn acgcctgtcc tttngeccca gaacctgctg tcttgtagac 120
ccaccagcag cagggctgcc gcgntgggcg tctcgatggg gcctgggtgg tcttgctgctg 180
ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240
ccctgcgccc ccctgtatga tgcacagccg agccatgggt cggggcaagc gccaggccac 300
tgcccactgc cccaacagct atgttaataa caatgacatc taccaggtca ctctgtctta 360
ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420
agccctcatg gaggtgcatg aggacttctt cctatacaag ggaggcatct acagccacac 480
gccagtgagc cttgggaggc cagagagata ccgccggcat gggaccact cag 533

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 14
ttcgaggcct ctgagaagtg gccc 24

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 15
ggcggatatct ctctggcctc cc 22

<210> 16
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 16
ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg 50

<210> 17
<211> 960
<212> DNA
<213> Homo sapiens

<400> 17
gctgcttgcc ctgttgatgg caggcttggc cctgcagcca ggcactgccc tgctgtgcta 60
ctcttgcaaa gccaggtga gcaacgagga ctgcctgcag gtggagaact gcaccagct 120
gggggagcag tgctggaccg cgcgcatccg cgagttggc ctctgaccg tcatcagcaa 180

```

aggctgcagc ttgaactgcg tggatgactc acaggactac tacgtgggca agaagaacat 240
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgccctgc agccggctgc 300
cgccatcctt gcgctgctcc ctgcactcgg cctgctgctc tggggaccgc gccagctata 360
ggctctgggg ggccccgctg cagcccacac tgggtgtggt gccccaggcc tctgtgccac 420
tcctcacaga cctggcccag tgggagcctg tcctggttcc tgaggcacat cctaacgcaa 480
gtctgaccat gtatgtctgc acccctgtcc cccaccctga ccctcccatg gccctctcca 540
ggactccac cccgcagatc agctctagt acacagatcc gcctgcagat ggcccccca 600
accctctctg ctgctgtttc catggcccag cattctccac ccttaaccct gtgctcaggc 660
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc caggtctggt 720
ccgtggtgtc cccgcacccc agcaggggac aggcactcag gagggcccag taaaggctga 780
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctccctg 900
aatggcagcc tgagcacagc gtaggccctt aataaacacc tgttgataa gccaaaaaaa 960

```

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

```

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
 1              5              10              15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
          20              25              30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
      35              40              45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50              55              60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65              70              75              80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
          85              90              95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
      100              105              110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
      115              120              125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
      130              135              140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
      145              150              155              160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
          165              170              175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
      180              185

```

<210> 19

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 19
tgctgtgcta ctcttgcaaa gccc 24

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 20
tgcacaagtc ggtgtcacag cacg 24

<210> 21
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 21
agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg 44

<210> 22
<211> 1200
<212> DNA
<213> Homo sapiens

<400> 22
cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgcccac acctcactct 60
gtgcttacag ctgctgattc tctgctgtca aactcagtac gtgagggacc agggcgccat 120
gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
caagcacgtg caggtcaccg ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt 240
tgccaagctc atagtggaga cggacacggt tggcagccgg gttcgcatca aaggggctga 300
gagtgagaag tacatctgta tgaacaagag gggcaagctc atcggaagc ccagcgggaa 360
gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg ccttccagaa 420
cgcccggcac gagggctggg tcatggcctt cacgcggcag gggcgggccc gccaggcttc 480
ccgagccgc cagaaccagc gcgaggccca cttcatcaag cgctctacc aaggccagct 540
gcccttcccc aaccacgccc agaagcagaa gcagttcgag tttgtgggct ccgccccac 600
ccgcccggacc aagcgcacac ggcgggccca gccctcag tagtctggga ggcagggggc 660
agcagccctt gggccgcctc cccacccctt tcccttctta atccaaggac tgggctgggg 720
tggcgggagg ggagccagat ccccgagggg ggaccctgag ggccgcgaag catccgagcc 780
cccagctggg aaggggcagg ccggtgcccc agggcgggct ggcacagtgc ccccttccc 840
gacgggtggc aggcctgga gaggaactga gtgtcaccct gatctcaggc caccagcctc 900
tgccggcctc ccagccgggc tcctgaagcc cgctgaaagg tcagcgactg aaggccttgc 960

agacaaccgt ctggagggtg ctgtcctcaa aatctgcttc tcggatctcc ctcagtctgc 1020
 cccagcccc caaactcctc ctggctagac tntaggaagg gacttttggt tgtttgtttg 1080
 tttcagggaaa aaagaaaggg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140
 acgaccagg cctgcacccc accccaact cccagccccg gaataaaacc attttcctgc 1200

<210> 23
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 23
 Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
 1 5 10 15
 Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
 20 25 30
 Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
 35 40 45
 Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
 50 55 60
 Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65 70 75 80
 Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
 85 90 95
 Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
 100 105 110
 Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
 115 120 125
 Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
 130 135 140
 Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
 145 150 155 160
 Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
 165 170 175
 His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
 180 185 190
 Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
 195 200 205

<210> 24
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

28

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 25

ccggtgacct gcacgtgctt gccca

24

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<220>

<221> modified_base

<222> (21)..(21)

<223> a, t, c or g

<400> 26

gcggatctgc gcgctgctca nctggtcggt catggcgccc t

41

<210> 27

<211> 2479

<212> DNA

<213> Homo sapiens

<400> 27

```
acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60
aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120
ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
tccagtcatt ttgattttgc tgtttatatt ttttttcttt ttctttttcc caccacattg 240
tattttatatt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300
cttttttccct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420
gcttgacctc agtgccctctt gggatcccgg agggcgtaac cgtactctac ctccacaaca 480
accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg 540
tctacctgta tggcaaccaaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600
ttctccattt gcaggaaaaac aatattcaga ccatttcacg ggctgctctt gcccagctct 660
tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720
gggccttccg ggaggctatt agcctcaaat tgttgttttt gtctaagaat cacctgagca 780
gtgtgcctgt tgggcttccct gtggacttgc aagagctgag agtggatgaa aatcgaattg 840
ctgtcatatc cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900
ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960
aggaattttc aattgtacgt aattcgctgt cccacctcc tcccgatctc ccaggtacgc 1020
```

```

atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080
caaactctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140
aaggggtttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200
tttgtgactg cagtattaaa tgggtcacag aatggctcaa atatatccct tcatctctca 1260
acgtgcgggg tttcatgtgc caaggctcctg aacaagtcgg ggggatggcc gtcaggggaat 1320
taaatatgaa tcttttgtcc tgtcccacca cgaccccggt cctgcctctc ttcaccccag 1380
ccccaaagta agcttctccg accactcagc ctcccaccct ctctattcca aaccctagca 1440
gaagctacac gcctccaact cctaccacat cgaaacttcc cagcattcct gactgggatg 1500
gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca taaaaactca 1620
catgggtgaa aatgggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680
gtgagaagca acacctgagc ctggttaact tagagccccg atccacctat cggatttggt 1740
tagtgccact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800
ccacccatgc ctcttatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860
cgtcccacag catgggctcc ccttttctgc tggcggggtt gatcgggggc gcggtgatat 1920
ttgtgctggt ggtcttgctc agcgtctttt gctggcatat gcacaaaag gggcgctaca 1980
cctcccagaa gtggaaatac aaccggggcc ggcgaaaga tgattattgc gaggcaggca 2040
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100
ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc ccaaattggg 2160
gcattaatta cacagactgc catatcccca acaacatgcy atactgcaac agcagcgtgc 2220
cagacctgga gcaactgcat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280
tagactcttg agaacacact cgtgtgtgca cataaagaca cgcagattac atttgataaa 2340
tgttacacag atgcatttgt gcatttgaat actctgtaat ttatacgggt tactatataa 2400
tgggatttaa aaaaagtgc atcttttcta tttcaagtta attacaaaca gttttgtaac 2460
tctttgcttt ttaaattctt
2479

```

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

```

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
  1              5              10              15

```

```

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
      20              25              30

```

```

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
      35              40              45

```

```

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
      50              55              60

```

```

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
      65              70              75              80

```

```

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
      85              90              95

```

```

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
      100              105              110

```

```

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
      115              120              125

```

```

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser

```

130					135					140					
Ile	Ser	Thr	Val	Gly	Val	Glu	Asp	Gly	Ala	Phe	Arg	Glu	Ala	Ile	Ser
145					150					155					160
Leu	Lys	Leu	Leu	Phe	Leu	Ser	Lys	Asn	His	Leu	Ser	Ser	Val	Pro	Val
				165					170					175	
Gly	Leu	Pro	Val	Asp	Leu	Gln	Glu	Leu	Arg	Val	Asp	Glu	Asn	Arg	Ile
			180					185					190		
Ala	Val	Ile	Ser	Asp	Met	Ala	Phe	Gln	Asn	Leu	Thr	Ser	Leu	Glu	Arg
		195					200					205			
Leu	Ile	Val	Asp	Gly	Asn	Leu	Leu	Thr	Asn	Lys	Gly	Ile	Ala	Glu	Gly
	210					215					220				
Thr	Phe	Ser	His	Leu	Thr	Lys	Leu	Lys	Glu	Phe	Ser	Ile	Val	Arg	Asn
225					230					235					240
Ser	Leu	Ser	His	Pro	Pro	Pro	Asp	Leu	Pro	Gly	Thr	His	Leu	Ile	Arg
				245					250					255	
Leu	Tyr	Leu	Gln	Asp	Asn	Gln	Ile	Asn	His	Ile	Pro	Leu	Thr	Ala	Phe
			260					265					270		
Ser	Asn	Leu	Arg	Lys	Leu	Glu	Arg	Leu	Asp	Ile	Ser	Asn	Asn	Gln	Leu
		275					280					285			
Arg	Met	Leu	Thr	Gln	Gly	Val	Phe	Asp	Asn	Leu	Ser	Asn	Leu	Lys	Gln
	290					295					300				
Leu	Thr	Ala	Arg	Asn	Asn	Pro	Trp	Phe	Cys	Asp	Cys	Ser	Ile	Lys	Trp
305						310				315					320
Val	Thr	Glu	Trp	Leu	Lys	Tyr	Ile	Pro	Ser	Ser	Leu	Asn	Val	Arg	Gly
				325					330					335	
Phe	Met	Cys	Gln	Gly	Pro	Glu	Gln	Val	Arg	Gly	Met	Ala	Val	Arg	Glu
			340					345					350		
Leu	Asn	Met	Asn	Leu	Leu	Ser	Cys	Pro	Thr	Thr	Thr	Pro	Gly	Leu	Pro
		355					360					365			
Leu	Phe	Thr	Pro	Ala	Pro	Ser	Thr	Ala	Ser	Pro	Thr	Thr	Gln	Pro	Pro
	370					375					380				
Thr	Leu	Ser	Ile	Pro	Asn	Pro	Ser	Arg	Ser	Tyr	Thr	Pro	Pro	Thr	Pro
385					390					395					400
Thr	Thr	Ser	Lys	Leu	Pro	Thr	Ile	Pro	Asp	Trp	Asp	Gly	Arg	Glu	Arg
				405					410					415	
Val	Thr	Pro	Pro	Ile	Ser	Glu	Arg	Ile	Gln	Leu	Ser	Ile	His	Phe	Val
			420					425					430		
Asn	Asp	Thr	Ser	Ile	Gln	Val	Ser	Trp	Leu	Ser	Leu	Phe	Thr	Val	Met

435					440					445						
Ala	Tyr	Lys	Leu	Thr	Trp	Val	Lys	Met	Gly	His	Ser	Leu	Val	Gly	Gly	
450					455					460						
Ile	Val	Gln	Glu	Arg	Ile	Val	Ser	Gly	Glu	Lys	Gln	His	Leu	Ser	Leu	
465					470					475					480	
Val	Asn	Leu	Glu	Pro	Arg	Ser	Thr	Tyr	Arg	Ile	Cys	Leu	Val	Pro	Leu	
485					490					495						
Asp	Ala	Phe	Asn	Tyr	Arg	Ala	Val	Glu	Asp	Thr	Ile	Cys	Ser	Glu	Ala	
500					505					510						
Thr	Thr	His	Ala	Ser	Tyr	Leu	Asn	Asn	Gly	Ser	Asn	Thr	Ala	Ser	Ser	
515					520					525						
His	Glu	Gln	Thr	Thr	Ser	His	Ser	Met	Gly	Ser	Pro	Phe	Leu	Leu	Ala	
530					535					540						
Gly	Leu	Ile	Gly	Gly	Ala	Val	Ile	Phe	Val	Leu	Val	Val	Leu	Leu	Ser	
545					550					555					560	
Val	Phe	Cys	Trp	His	Met	His	Lys	Lys	Gly	Arg	Tyr	Thr	Ser	Gln	Lys	
565					570					575						
Trp	Lys	Tyr	Asn	Arg	Gly	Arg	Arg	Lys	Asp	Asp	Tyr	Cys	Glu	Ala	Gly	
580					585					590						
Thr	Lys	Lys	Asp	Asn	Ser	Ile	Leu	Glu	Met	Thr	Glu	Thr	Ser	Phe	Gln	
595					600					605						
Ile	Val	Ser	Leu	Asn	Asn	Asp	Gln	Leu	Leu	Lys	Gly	Asp	Phe	Arg	Leu	
610					615					620						
Gln	Pro	Ile	Tyr	Thr	Pro	Asn	Gly	Gly	Ile	Asn	Tyr	Thr	Asp	Cys	His	
625					630					635					640	
Ile	Pro	Asn	Asn	Met	Arg	Tyr	Cys	Asn	Ser	Ser	Val	Pro	Asp	Leu	Glu	
645					650					655						
His	Cys	His	Thr													
660																

<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c

<210> 30

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30
gcaggacaac cagataaacc ac 22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31
acgcagattt gagaaggctg tc 22

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32
ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac 46

<210> 33
<211> 3449
<212> DNA
<213> Homo sapiens

<400> 33
acttgagca agcggcgggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60
cgctccccc gagcgaatccc cgaggagagc cgcgccctc ggcgaggcga agaggccgac 120
gaggaagacc cgggtggctg cgccctgcc tcgcttccca ggcgccggcg gctgcagcct 180
tgccctctt gctcgcttg aaaatggaaa agatgctcgc aggtgcttt ctgctgatcc 240
tcggacagat cgtcctctc cctgccgagg ccaggagcgc gtcacgtggg aggtccatct 300
ctaggggcag acacgctcgg acccaccgc agacggccct tctggagagt tcctgtgaga 360
acaagcgggc agacctggtt ttcatcattg acagctctcg cagtgtcaac acccatgact 420
atgcaaaggc caaggagttc atcgtggaca tcttgcaatt cttggacatt ggtcctgatg 480
tcacccgagt gggcctgctc caatatggca gcactgtcaa gaatgagttc tccctcaaga 540
ccttcaagag gaagtccgag gtggagcgtg ctgtcaagag gatgcggcat ctgtccacgg 600
gcaccatgac tgggctggcc atccagtatg ccctgaacat cgcattctca gaagcagagg 660
gggcccggcc cctgagggag aatgtgccac gggtcataat gatcgtgaca gatgggagac 720
ctcaggactc cgtggccgag gtggctgcta aggcacggga cacgggcac ctaatctttg 780
ccattggtgt gggccaggta gacttcaaca ccttgaagtc cattgggagt gagcccatg 840
aggaccatgt cttccttggt gccaatctca gccagattga gacgctgacc tccgtgttcc 900
agaagaagtt gtgcacggcc cacatgtgca gcaccctgga gcataactgt gccacttct 960

gcatcaacat	ccctgggtca	tacgtctgca	ggtgcaaaca	aggctacatt	ctcaactcgg	1020
atcagacgac	ttgcagaatc	caggatctgt	gtgccatgga	ggaccacaac	tgtgagcagc	1080
tctgtgtgaa	tgtgccgggc	tccttcgtct	gccagtgcct	cagtggctac	gccctggctg	1140
aggatgggaa	gaggtgtgtg	gctgtggact	actgtgcctc	agaaaaccac	ggatgtgaac	1200
atgagtgtgt	aaatgctgat	ggctcctacc	tttgccagtg	ccatgaagga	tttgctctta	1260
accagatgta	aaaaacgtgc	acaaggatca	actactgtgc	actgaacaaa	ccgggctgtg	1320
agcatgagtgt	cgtcaacatg	gaggagagct	actactgccg	ctgccaccgt	ggctacactc	1380
tggaccccaa	tggcaaaacc	tgcagccgag	tggaccactg	tgcacagcag	gaccatggct	1440
gtgagcagct	gtgtctgaac	acggaggatt	ccttcgtctg	ccagtgtctca	gaaggcttcc	1500
tcatcaacga	ggacctcaag	acctgtctcc	gggtggatta	ctgcctgtctg	agtgaccatg	1560
gttgtgaata	ctcctgtgtc	aacatggaca	gaccccttgc	ctgtcagtgt	cctgaggggac	1620
acgtgtctccg	cagcgatggg	aagacgtgtg	caaaattgga	ctcttgtgtc	ctggggggacc	1680
acggtttgtga	acattcgtgt	gtaagcagtg	aagattcgtt	tgtgtgccag	tgctttgaag	1740
gttatatact	ccgtgaagat	ggaaaaacct	gcagaaggaa	agatgtctgc	caagctatag	1800
accatggctg	tgaacacatt	tgtgtgaaca	gtgacgactc	atacacgtgc	gagtgtcttg	1860
agggattccg	gctcgtctgag	gatgggaaac	gctgccgaag	gaaggatgtc	tgcaaatcaa	1920
cccaccatgg	ctgcgaacac	atthgtgtta	ataatgggaa	ttcctacatc	tgcaaatgct	1980
cagaggggatt	tgttctagct	gaggacggaa	gacggtgcaa	gaaatgcact	gaaggcccaa	2040
ttgacctggt	ctttgtgatc	gatggatcca	agagtcttgg	agaagagaat	tttgaggctg	2100
tgaagcagtt	tgtcactgga	attatagatt	ccttgacaat	ttccccaaa	gccgctcgag	2160
tggggctgct	ccagtattcc	acacaggtcc	acacagagtt	cactctgaga	aacttcaact	2220
cagccaaaaga	catgaaaaaa	gccgtggccc	acatgaaata	catgggaaag	ggctctatga	2280
ctgggctggc	cctgaaacac	atgtttgaga	gaagttttac	ccaaggagaa	ggggccaggc	2340
ccctttccac	aagggtgccc	agagcagcca	ttgtgttcac	cgacggacgg	gctcaggatg	2400
acgtctccga	gtgggccagt	aaagccaagg	ccaatggtat	cactatgtat	gctgttgggg	2460
taggaaaagc	cattgaggag	gaactacaag	agattgcctc	tgagcccaca	aacaagcatc	2520
tcttctatgc	cgaagacttc	agcacaatgg	atgagataag	tgaaaaactc	aagaaaggca	2580
tctgtgaagc	tctagaagac	tccgatggaa	gacaggactc	tccagcaggg	gaactgccaa	2640
aaacggtcca	acagccaaca	gaatctgagc	cagtcaccat	aaatatccaa	gacctacttt	2700
cctgtttctaa	ttttgcagtg	caacacagat	atctgtttga	agaagacaat	cttttacggg	2760
ctacacaaaa	gctttcccat	tcaacaaaac	cttcaggaag	ccctttggaa	gaaaaacacg	2820
atcaatgcaa	atgtgaaaac	cttataatgt	tccagaacct	tgcaaacgaa	gaagtaagaa	2880
aattaacaca	gcgcttagaa	gaaatgacac	agagaatgga	agccctggaa	aatcgccctga	2940
gatacagatg	aagattagaa	atcgcgacac	atthgtagtc	attgtatcac	ggattacaat	3000
gaacgcagtg	cagagcccca	aagctcaggc	tattgttaaa	tcaataatgt	tgtgaagtaa	3060
aacaatcagt	actgagaaac	ctggtttgcc	acagaacaaa	gacaagaagt	atacactaac	3120
ttgtataaat	ttatctagga	aaaaaatcct	tcagaattct	aagatgaatt	taccaggtga	3180
gaatgaataa	gctatgcaag	gtatthttgt	atatactgtg	gacacaactt	gcttctgcct	3240
catcctgcct	tagtgtgcaa	tctcatttga	ctatacgata	aagtttgcac	agtcttactt	3300
ctgtagaaca	ctggccatag	gaaatgctgt	ttttttgtac	tggactttac	cttgatatat	3360
gtatatggat	gtatgcataa	aatcatagga	catatgtact	tgtggaacaa	gttggttttt	3420
ttatacaata	ttaaaattca	ccacttcag				3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34.

Met	Glu	Lys	Met	Leu	Ala	Gly	Cys	Phe	Leu	Leu	Ile	Leu	Gly	Gln	Ile
1				5					10					15	

Val	Leu	Leu	Pro	Ala	Glu	Ala	Arg	Glu	Arg	Ser	Arg	Gly	Arg	Ser	Ile
			20					25					30		

Ser	Arg	Gly	Arg	His	Ala	Arg	Thr	His	Pro	Gln	Thr	Ala	Leu	Leu	Glu
		35					40					45			

Ser	Ser	Cys	Glu	Asn	Lys	Arg	Ala	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser	50	55	60
Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile	65	70	75
Val	Asp	Ile	Leu	Gln	Phe	Leu	Asp	Ile	Gly	Pro	Asp	Val	Thr	Arg	Val	85	90	95
Gly	Leu	Leu	Gln	Tyr	Gly	Ser	Thr	Val	Lys	Asn	Glu	Phe	Ser	Leu	Lys	100	105	110
Thr	Phe	Lys	Arg	Lys	Ser	Glu	Val	Glu	Arg	Ala	Val	Lys	Arg	Met	Arg	115	120	125
His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu	130	135	140
Asn	Ile	Ala	Phe	Ser	Glu	Ala	Glu	Gly	Ala	Arg	Pro	Leu	Arg	Glu	Asn	145	150	155
Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser	165	170	175
Val	Ala	Glu	Val	Ala	Ala	Lys	Ala	Arg	Asp	Thr	Gly	Ile	Leu	Ile	Phe	180	185	190
Ala	Ile	Gly	Val	Gly	Gln	Val	Asp	Phe	Asn	Thr	Leu	Lys	Ser	Ile	Gly	195	200	205
Ser	Glu	Pro	His	Glu	Asp	His	Val	Phe	Leu	Val	Ala	Asn	Phe	Ser	Gln	210	215	220
Ile	Glu	Thr	Leu	Thr	Ser	Val	Phe	Gln	Lys	Lys	Leu	Cys	Thr	Ala	His	225	230	235
Met	Cys	Ser	Thr	Leu	Glu	His	Asn	Cys	Ala	His	Phe	Cys	Ile	Asn	Ile	245	250	255
Pro	Gly	Ser	Tyr	Val	Cys	Arg	Cys	Lys	Gln	Gly	Tyr	Ile	Leu	Asn	Ser	260	265	270
Asp	Gln	Thr	Thr	Cys	Arg	Ile	Gln	Asp	Leu	Cys	Ala	Met	Glu	Asp	His	275	280	285
Asn	Cys	Glu	Gln	Leu	Cys	Val	Asn	Val	Pro	Gly	Ser	Phe	Val	Cys	Gln	290	295	300
Cys	Tyr	Ser	Gly	Tyr	Ala	Leu	Ala	Glu	Asp	Gly	Lys	Arg	Cys	Val	Ala	305	310	315
Val	Asp	Tyr	Cys	Ala	Ser	Glu	Asn	His	Gly	Cys	Glu	His	Glu	Cys	Val	325	330	335
Asn	Ala	Asp	Gly	Ser	Tyr	Leu	Cys	Gln	Cys	His	Glu	Gly	Phe	Ala	Leu	340	345	350

Asn	Pro	Asp	Glu	Lys	Thr	Cys	Thr	Arg	Ile	Asn	Tyr	Cys	Ala	Leu	Asn	355	360	365
Lys	Pro	Gly	Cys	Glu	His	Glu	Cys	Val	Asn	Met	Glu	Glu	Ser	Tyr	Tyr	370	375	380
Cys	Arg	Cys	His	Arg	Gly	Tyr	Thr	Leu	Asp	Pro	Asn	Gly	Lys	Thr	Cys	385	390	395
Ser	Arg	Val	Asp	His	Cys	Ala	Gln	Gln	Asp	His	Gly	Cys	Glu	Gln	Leu	405	410	415
Cys	Leu	Asn	Thr	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Ser	Glu	Gly	Phe	420	425	430
Leu	Ile	Asn	Glu	Asp	Leu	Lys	Thr	Cys	Ser	Arg	Val	Asp	Tyr	Cys	Leu	435	440	445
Leu	Ser	Asp	His	Gly	Cys	Glu	Tyr	Ser	Cys	Val	Asn	Met	Asp	Arg	Ser	450	455	460
Phe	Ala	Cys	Gln	Cys	Pro	Glu	Gly	His	Val	Leu	Arg	Ser	Asp	Gly	Lys	465	470	475
Thr	Cys	Ala	Lys	Leu	Asp	Ser	Cys	Ala	Leu	Gly	Asp	His	Gly	Cys	Glu	485	490	495
His	Ser	Cys	Val	Ser	Ser	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Phe	Glu	500	505	510
Gly	Tyr	Ile	Leu	Arg	Glu	Asp	Gly	Lys	Thr	Cys	Arg	Arg	Lys	Asp	Val	515	520	525
Cys	Gln	Ala	Ile	Asp	His	Gly	Cys	Glu	His	Ile	Cys	Val	Asn	Ser	Asp	530	535	540
Asp	Ser	Tyr	Thr	Cys	Glu	Cys	Leu	Glu	Gly	Phe	Arg	Leu	Ala	Glu	Asp	545	550	555
Gly	Lys	Arg	Cys	Arg	Arg	Lys	Asp	Val	Cys	Lys	Ser	Thr	His	His	Gly	565	570	575
Cys	Glu	His	Ile	Cys	Val	Asn	Asn	Gly	Asn	Ser	Tyr	Ile	Cys	Lys	Cys	580	585	590
Ser	Glu	Gly	Phe	Val	Leu	Ala	Glu	Asp	Gly	Arg	Arg	Cys	Lys	Lys	Cys	595	600	605
Thr	Glu	Gly	Pro	Ile	Asp	Leu	Val	Phe	Val	Ile	Asp	Gly	Ser	Lys	Ser	610	615	620
Leu	Gly	Glu	Glu	Asn	Phe	Glu	Val	Val	Lys	Gln	Phe	Val	Thr	Gly	Ile	625	630	635
Ile	Asp	Ser	Leu	Thr	Ile	Ser	Pro	Lys	Ala	Ala	Arg	Val	Gly	Leu	Leu	645	650	655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800
 Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815
 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830
 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845
 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860
 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880
 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
 885 890 895
 Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
 900 905 910
 Arg Tyr Arg
 915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

ggagccgccc	tgggtgtcag	cggtctcggt	cccgcgcacg	ctccggccgt	cgcgagcct	60
cggcacctgc	aggtccgtgc	gtcccgcggc	tggcgcccct	gactccgtcc	cggccagggg	120
gggccatgat	tccctccccg	gggcccctgg	tgaccaactt	gctgcggttt	ttgttcctgg	180
ggctgagtgc	cctcgcgccc	ccctcgcggg	cccagctgca	actgcacttg	cccgccaacc	240
ggttgcaggc	ggtggaggga	ggggaagtgg	tgcttcacgc	gtggtacacc	ttgcacgggg	300
aggtgtcttc	atcccagcca	tgggaggtgc	cctttgtgat	gtggttcttc	aaacagaaag	360
aaaaggagga	tcaggtgttg	tcctacatca	atggggtcac	aacaagcaaa	cctggagtat	420
ccttgggtcta	ctccatgccc	tcccgggaacc	tgtccctgcg	gctggagggt	ctccaggaga	480
aagactctgg	cccctacagc	tgctccgtga	atgtgcaaga	caaacaaggc	aaatctaggg	540
gccacagcat	caaaacctta	gaactcaatg	tactggttcc	tccagctcct	ccatcctgcc	600
gtctccaggg	tgtgccccat	gtgggggcaa	acgtgaccct	gagctgccag	tctccaagga	660
gtaagcccgc	tgtccaatac	cagtgggatc	ggcagcttcc	atccttccag	actttctttg	720
caccagcatt	agatgtcatc	cgtgggtcct	taagcctcac	caacctttcg	tcttccatgg	780
ctggagtcta	tgtctgcaag	gcccacaatg	aggtgggcac	tgcccaatgt	aatgtgacgc	840
tggaagtggg	cacagggcct	ggagctgcag	tgggtgctgg	agctgttgtg	ggtaccctgg	900
ttggactggg	gttgctggct	gggctggtcc	tcttgtagca	ccgcccgggc	aaggccctgg	960
aggagccagc	caatgatatc	aaggaggatg	ccattgctcc	ccggaccctg	ccctggccca	1020
agagctcaga	cacaatctcc	agaatggga	ccctttcttc	tgacacctcc	gcacgagccc	1080
tccggccacc	ccatggccct	cccaggcctg	gtgcattgac	ccccacgccc	agtctctcca	1140
gccaggccct	gccctcacca	agactgcccc	cgacagatgg	ggcccaccct	caaccaatat	1200

```

ccccatccc tgggtggggtt tcttcctctg gcttgagccg catgggtgct gtgcctgtga 1260
tgggtgcctgc ccagagtcaa gctggctctc tggatatgatg accccaccac tcattggcta 1320
aaggatttgg ggtctctcct tcctataaagg gtcacctcta gcacagaggc ctgagtcgatg 1380
ggaaagagtc aacttcctga cccttagtac tctgccccca cctctcttta ctgtgggaaa 1440
accatctcag taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500
attgggagga gcctccaccc acccctgact cctccttatg aagccagctg ctgaaattag 1560
ctactacca agagtgaggg gcagagactt ccagtcactg agtctcccag gcccccttga 1620
tctgtacccc acccctatct aacaccaccc ttgggtccca ctccagctcc ctgtattgat 1680
ataacctgtc aggctggctt ggtaggttt tactggggca gaggataggg aatctcttat 1740
taaaactaac atgaaatatg tgtgttttc atttgcaa ataaataaag atacataatg 1800
tttgtatgaa aaa 1813

```

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

```

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu
 1             5             10             15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
      20             25             30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
      35             40             45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
      50             55             60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
      65             70             75             80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
      85             90             95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
      100            105            110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
      115            120            125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
      130            135            140

Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
      145            150            155            160

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
      165            170            175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
      180            185            190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
      195            200            205

```


Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
 210 215 220
 Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
 225 230 235 240
 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
 245 250 255
 Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
 260 265 270
 Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
 275 280 285
 Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300
 Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320
 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335
 Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350
 Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365
 Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380
 Gln Ala Gly Ser Leu Val
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 41	
attgtgggcc ttgcagacat agac	24
<210> 42	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 42	
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc	50
<210> 43	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 43	
gtgtgacaca gcgtgggc	18
<210> 44	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 44	
gaccggcagg cttctgcg	18
<210> 45	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 45	
cagcagcttc agccaccagg agtgg	25
<210> 46	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 46

ctgagccgtg ggctgcagtc tcgc

24

<210> 47

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 47

ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc

45

<210> 48

<211> 2822

<212> DNA

<213> Homo sapiens

<400> 48

cgccaccact	gcggccaccg	ccaatgaaac	gcctcccgct	cctagtgggtt	ttttccactt	60
tggttgaattg	ttcctatact	caaaattgca	ccaagacacc	ttgtctccca	aatgcaaaat	120
gtgaaatacg	caatggaatt	gaagcctgct	attgcaacat	gggattttca	ggaaatgggtg	180
tcacaatttg	tgaagatgat	aatgaatgtg	gaaattttaac	tcagtcctgt	ggcgaaaatg	240
ctaattgcac	taacacagaa	ggaagttatt	attgtatgtg	tgtacctggc	ttcagatcca	300
gcagtaacca	agacaggttt	atcactaatg	atggaaccgt	ctgtatagaa	aatgtgaatg	360
caaactgcc	tttagataat	gtctgtatag	ctgcaaatat	taataaaaact	ttaacaaaaa	420
tcagatccat	aaaagaacct	gtggctttgc	tacaagaagt	ctatagaaat	tctgtgacag	480
atctttcacc	aacagatata	attacatata	tagaaatatt	agctgaatca	tcttcattac	540
taggttacaa	gaacaacact	atctcagcca	aggacaccct	ttctaactca	actcttactg	600
aatttgtaaa	aaccgtgaat	aattttgttc	aaagggatac	atltgtagtt	tgggacaagt	660
tatctgtgaa	tcataggaga	acacatctta	caaaactcat	gcacactgtt	gaacaagcta	720
ctttaaggat	atcccagagc	ttccaaaaga	ccacagagtt	tgatacaaat	tcaacggata	780
tagctctcaa	agttttcttt	tttgattcat	ataacatgaa	acatattcat	cctcatatga	840
atatggatgg	agactacata	aatatatttc	caaagagaaa	agctgcatat	gattcaaatg	900
gcaatgtttg	attgtcattt	ttatattata	agagtattgg	tcctttgctt	tcattcatctg	960
acaacttctt	attgaaacct	caaaattatg	ataattctga	agaggaggaa	agagtcatat	1020
cttcagtaat	ttcagttctca	atgagctcaa	acccaccac	attatatgaa	cttgaaaaaa	1080
taacattttac	attaagtcac	cgaaagggtca	cagataggta	taggagtcta	tgtgcatttt	1140
ggaattactc	acctgatacc	atgaatggca	gctgggtcttc	agagggctgt	gagctgacat	1200
actcaaatga	gaccacacac	tcattgccgt	gtaatcacct	gacacatttt	gcaattttga	1260
tgtcctctgg	tccttccatt	ggtattaaag	attataatat	tcttacaagg	atcactcaac	1320
taggaataat	tatttctactg	atttgtcttg	ccatatgcat	ttttaccttc	tgggttcttca	1380
gtgaaattca	aagcaccagg	acaacaattc	acaaaaatct	ttgctgtagc	ctatttcttg	1440
ctgaacttgt	ttttcttggt	gggatcaata	caaatactaa	taagctcttc	tgttcaatca	1500
ttgccggact	gctacactac	ttcttttttag	ctgcttttgc	atggatgtgc	attgaaggca	1560
tacatctcta	tctcattggt	gtgggtgtca	tctacaacaa	gggatttttg	cacaagaatt	1620
tttatatctt	tggctatcta	agcccagccg	tggtagttgg	atlttcggca	gcactaggat	1680
acagatatta	tggcacaacc	aaagtatggt	ggcttagcac	cgaaaacaac	tttattttgga	1740
gttttatagg	accagcatgc	ctaattcatc	ttgttaatct	cttggccttt	ggagtcatca	1800
tatacaaagt	ttttcgtcac	actgcagggt	tgaaccagaa	agtttagttgc	tttgagaaca	1860
taaggtcttg	tgcaagagga	gccctcgctc	ttctgttctc	tctcggcacc	acctggatct	1920
ttgggggtct	ccatgtttgtg	cacgcacatc	tggttacagc	ttacctcttc	acagtcagca	1980

```

atgctttcca ggggatgttc atttttttat tcctgtgtgt tttatctaga aagattcaag 2040
aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100
agagaatggt ggataattac aactgcacaa aaataaaaaat tccaagctgt ggatgaccaa 2160
tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtattttta 2220
atcagttttt ctgtttatgc tataggaact gtagataata aggtaaaatt atgtatcata 2280
tagatatact atgtttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
ggaaagtaat tggtttctca ggagtgatat cactgcaccc aaggaaagat tttctttcta 2400
acacgagaag tatatgaatg tcctgaagga aaccactggc ttgatatttc tgtgactcgt 2460
gttgcccttg aaactagtcc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
cataagagaa tgaaggggca gaatatcaaa cagtgaaaag ggaatgataa gatgtatttt 2580
gaatgaactg ttttttctgt agactagctg agaaattggt gacataaaat aaagaattga 2640
agaaacacat tttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700
agacttctgt ttgctaaatc tgtttctttt tctaattatt taaaaaaaaa aaaaagggtt 2760
acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aa

```

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

```

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
  1               5               10              15

```

```

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20              25              30

```

```

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35              40              45

```

```

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50              55              60

```

```

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65              70              75              80

```

```

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85              90              95

```

```

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
     100              105              110

```

```

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
     115              120              125

```

```

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
     130              135              140

```

```

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
     145              150              155              160

```

```

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
     165              170              175

```

```

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr
     180              185              190

```

Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val	195	200	205
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys	210	215	220
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe	225	230	235
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys	245	250	255
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met	260	265	270
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala	275	280	285
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser	290	295	300
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln	305	310	315
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile	325	330	335
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys	340	345	350
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser	355	360	365
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp	370	375	380
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser	385	390	395
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly	405	410	415
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln	420	425	430
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr	435	440	445
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys	450	455	460
Asn	Leu	Cys	Cys	Ser	Leu	Phe	Leu	Ala	Glu	Leu	Val	Phe	Leu	Val	Gly	465	470	475
Ile	Asn	Thr	Asn	Thr	Asn	Lys	Leu	Phe	Cys	Ser	Ile	Ile	Ala	Gly	Leu	485	490	495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675 680 685

Leu Arg
690

<210> 50

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (61)..(61)

<223> a, t, c or g

<400> 50

tggaacata tcctccctca tatgaatat gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaatggca atgttgcagt tgcattttta tattataaga 120
gtattggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcatcg aaaggtcaca 300
gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360

tgggtcttcag agggctgtga gctgacatac tcaaatagaga cccacacctc atgccgctgt 420
 aatcacctga cacattttgc aattttgatg tcctctgggc cttccattgg tattaagat 480
 tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
 atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 57

atgagacca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60
cgctaagcga ggcctcctcc tcccgcagat ccgaacggcc tgggcggggt caccgccgct 120
gggacaagaa gccgcgcct gcctgcccgg gcccgggag ggggctggg ctggggccgg 180
aggcggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240
tgctcgggtg tcttgggcac ctaccctggg ggcccgtaa gcgctactat ataaggctgc 300
cgggccggag ccgccgcgcc gtcagagcag gagcgctgcg tccaggatct agggccacga 360
ccatcccaac ccggcactca cagccccgca gcgcacccg gtcgccgcc agcctccgc 420
acccccatcg ccggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480
ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctgc 540
cttctcggac gcggggcccc acgtgacta cggtggggc gacccatcc gcctgcggca 600
cctgtacacc tccggcccc acgggtctc cagctgctt ctgcgcaccc gtgccgacgg 660
cgctcgtggac tgccgcggg gccagagcgc gcacagtgt ctggagatca aggcagtcgc 720
tctgcggacc gtggccatca agggcgtgca cagcgtgcg tacctctgca tgggcgccga 780
cggcaagatg caggggctgc ttcagtact ggaggaagac tgtgctttcg aggaggagat 840
ccgccagat ggctacaatg tgtaccgatc cgagaagcac cgcctcccgg tctccctgag 900
cagtgcctaa cagcggcagc tgtacaagaa cagaggctt cttccactct ctcatcttct 960
gcccattgctg cccatggtcc cagaggagcc tgaggacct agggggccact tggaatctga 1020
catgttctct tcgcccttg agaccgacag catggacca tttgggcttg tcaccggact 1080
ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140


```

tgctgccagg ggctgtggta cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200
agtccacggt ctgttttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260
tccattggca gtgccagttt ctagccaata gacttgtctg atcataacat tgtaagcctg 1320
tagcttgccc agctgctgcc tgggccccca ttctgtctcc tcgaggttgc tggacaagct 1380
gctgcactgt ctcagttctg cttgaatacc tccatcgatg gggaactcac ttcctttgga 1440
aaaattctta tgtcaagctg aaattctcta atttttctc atcacttccc caggagcagc 1500
cagaagacag gcagtagttt taatttcagg aacaggatgat ccactctgta aaacagcagg 1560
taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620
cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680
ggagtagggg aagcctggag cccactcca gccctgggac aacttgagaa ttccccctga 1740
ggccagttct gtcatggatg ctgtcctgag aataacttgc tgtcccgggtg tcacctgctt 1800
ccatctccca gccaccagc cctctgccca cctcacatgc ctccccatgg attggggcct 1860
cccaggcccc ccaccttatg tcaacctgca cttcttggtc aaaaatcagg aaaagaaaag 1920
atgtgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagacctt 1980
gaaccctttc cccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040
tgtacatctc ttattttctt acattattta tgcccccaa ttatatttat gtatgtaagt 2100
gaggtttggt ttgtatatta aaatggagtt tgtttgt 2137

```

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
  1             5             10             15

```

```

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
          20             25             30

```

```

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
      35             40             45

```

```

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
      50             55             60

```

```

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
      65             70             75             80

```

```

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
          85             90             95

```

```

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
      100             105             110

```

```

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
      115             120             125

```

```

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
      130             135             140

```

```

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
      145             150             155             160

```

```

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
          165             170             175

```

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 61

gcctcccgtg ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 62

ccagtcggtg gacaagccca aa

22

<210> 63

<211> 1295

<212> DNA

<213> Homo sapiens

<400> 63

cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60
cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120
gctgctgctg cgctacctgg tggcgcctt gggctatcat aaggcctatg ggttttctgc 180
cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggtatatt tagcctgcaa 240
aaccctaaag aagactgttt cctccagatt agagtggaag aaactgggtc ggagtgtctc 300
ctttgtctac tatcaacaga ctcttcaagg tgatttttaa aatcgagctg agatgataga 360

```

tttcaatatc cggatcaaaa atgtgacaag aagtgatgcg gggaaatatc gttgtgaagt 420
tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaagtatt 480
agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggg 540
agagctacga tgtcaagaca aagaagggaa tccagctcct gaatacacat ggtttaagga 600
tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660
aatgaatata aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720
atattcctgt gaagcccgca attctgttgg atatcgagg tgcctggga aacgaatgca 780
agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840
ttccgtttgt ggccttggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900
ctccttcag aagagtaatt cttcatctaa agccacgaca atgagtgaaa atgtgcagtg 960
gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020
gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080
ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140
acccgggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200
cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260
tgtagaattc ttacaataaa tatagcttga tattc 1295

```

<210> 64

<211> 312

<212> PRT

<213> Homo sapiens

<400> 64

```

Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Leu Arg Tyr
  1             5             10             15

```

```

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
      20             25             30

```

```

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
      35             40             45

```

```

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
      50             55             60

```

```

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
      65             70             75             80

```

```

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
      85             90             95

```

```

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
      100            105            110

```

```

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
      115            120            125

```

```

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
      130            135            140

```

```

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
      145            150            155            160

```

```

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
      165            170            175

```

```

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met

```

180					185					190						
Asn	Thr	Lys	Thr	Gly	Thr	Leu	Gln	Phe	Asn	Thr	Val	Ser	Lys	Leu	Asp	
195					200					205						
Thr	Gly	Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Ser	Val	Gly	Tyr	Arg	Arg	
210					215					220						
Cys	Pro	Gly	Lys	Arg	Met	Gln	Val	Asp	Asp	Leu	Asn	Ile	Ser	Gly	Ile	
225					230					235					240	
Ile	Ala	Ala	Val	Val	Val	Val	Ala	Leu	Val	Ile	Ser	Val	Cys	Gly	Leu	
245					250					255						
Gly	Val	Cys	Tyr	Ala	Gln	Arg	Lys	Gly	Tyr	Phe	Ser	Lys	Glu	Thr	Ser	
260					265					270						
Phe	Gln	Lys	Ser	Asn	Ser	Ser	Ser	Lys	Ala	Thr	Thr	Met	Ser	Glu	Asn	
275					280					285						
Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Lys	Ala	Ala	Ala	
290					295					300						
Gly	Gly	Ser	Arg	Gly	Gln	Glu	Phe									
305					310											

<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 65

atcgttgtga agttagtgcc cc

22

<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 66

acctgcgata tccaacagaa ttg

23

<210> 67

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

48

<210> 68

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 68

gacatcgagg	gtgggctagc	actgaaactg	cttttcaaga	cgaggaagag	gaggagaaaag	60
agaaagaaga	ggaagatggt	gggcaacatt	tattttaacat	gctccacagc	ccggaccctg	120
gcatcatgct	gctattcctg	caaatactga	agaagcatgg	gattttaaata	ttttacttct	180
aaataaatga	attactcaat	ctcctatgac	catctataca	tactccacct	tcaaaaagta	240
catcaatatt	atatcattaa	ggaaatagta	accttctctt	ctccaatatg	catgacattt	300
ttggacaatg	caattgtggc	actggcactt	atttcagtga	agaaaaactt	tgtggttcta	360
tggcattcat	catttgacaa	atgcaagcat	cttccttata	aatcagctcc	tattgaactt	420
actagcactg	actgtggaat	ccttaagggc	ccattacatt	tctgaagaag	aaagctaaga	480
tgaaggcatg	gccaactcga	attcatgtgc	tacttggcct	agctatcact	acactagtac	540
aagctgtaga	taaaaaagtg	gattgtccac	ggttatgtac	gtgtgaaatc	aggccttggt	600
ttacacccag	atccatttat	atggaagcat	ctacagtggg	ttgtaatgat	ttaggtcttt	660
taactttccc	agccagattg	ccagctaaca	cacagattct	tctcctacag	actaacaata	720
ttgcaaaaat	tgaatactcc	acagactttc	cagtaaacct	tactggcctg	gatttatctc	780
aaaacaattt	atcttcagtc	accaatatta	atgtaaaaaa	gatgcctcag	ctcctttctg	840
tgtacctaga	ggaaaacaaa	cttactgaac	tgcctgaaaa	atgtctgtcc	gaactgagca	900
acttacaaga	actctatatt	aatcacaact	tgccttctac	aatttcacct	ggagccttta	960
ttggcctaca	taatcttctt	cgacttcatc	tcaattcaaa	tagattgcag	atgatcaaca	1020
gtaagtgggt	tgatgtctct	ccaaatctag	agattctgat	gattggggaa	aatccaatta	1080
tcagaatcaa	agacatgaac	tttaagcctc	ttatcaatct	tgcgagcctg	gttatagctg	1140
gtataaacct	cacagaaata	ccagataacg	ccttggttgg	actggaaaac	ttagaaagca	1200
tctcttttta	cgataacagg	cttattaaag	taccccatgt	tgctcttcaa	aaagttgtaa	1260
atctcaaatt	tttgatctta	aataaaaaatc	ctattaatag	aatacgaagg	ggtgatttta	1320
gcaatatgct	acacttaaaa	gagttgggga	taaataatat	gcctgagctg	atttccatcg	1380
atagtcttgc	tgtggataac	ctgccagatt	taagaaaaat	agaagctact	aacaacccta	1440
gattgtctta	cattcacccc	aatgcatttt	tcagactccc	caagctggaa	tcactcatgc	1500
tgaacagcaa	tgctctcagt	gccctgtacc	atgggtaccat	tgagtctctg	ccaaacctca	1560
aggaaatcag	catacacagt	aaccccatca	ggtgtgactg	tgatcatccg	tggatgaaca	1620
tgaacaaaac	caacattcga	ttcatggagc	cagattcact	gttttgcgtg	gaccacctg	1680
aatccaagg	tcagaatggt	cggcaagtgc	atttcaggga	catgatggaa	atttgtctcc	1740
ctcttatagc	tcctgagagc	tttccttcta	atctaaatgt	agaagctggg	agctatgttt	1800
cctttcactg	tagagctact	gcagaaccac	agcctgaaat	ctactggata	acaccttctg	1860
gtcaaaaact	cttgccctaat	accctgacag	acaagttcta	tgtccattct	gagggaacac	1920
tagatataaa	tggcgtaact	cccaaagaag	gggggtttata	tacttgtata	gcaactaacc	1980
tagttggcgc	tgacttgaag	tctgttatga	tcaaagtggg	tggatctttt	ccacaagata	2040
acaatggctc	tttgaatatt	aaaataagag	atattcaggc	caattcagtt	ttggtgtcct	2100
ggaaagcaag	ttctaaaatt	ctcaaactta	gtgttaaagt	gacagccttt	gtcaagactg	2160
aaaattctca	tgctgcgcaa	agtgtctgaa	taccatctga	tgtcaaggta	tataatctta	2220
ctcatctgaa	tccatcaact	gagtataaaa	tttgtattga	tattcccacc	atctatcaga	2280
aaaacagaaa	aaaatgtgta	aatgtcacca	ccaaagggtt	gcaccctgat	caaaaagagt	2340
atgaaaagaa	taataccaca	acacttatgg	cctgtcttgg	aggccttctg	gggattattg	2400
gtgtgatatg	tcttatcagc	tgccctctct	cagaaatgaa	ctgtgatggg	ggacacagct	2460
atgtgaggaa	ttacttacag	aaaccaacct	ttgcattagg	tgagctttat	cctcctctga	2520
taaatctctg	ggaagcagga	aaagaaaaaa	gtacatcact	gaaagtaaaa	gcaactgtta	2580
taggtttacc	aacaaatatg	tcctaaaaac	caccaaggaa	acctactcca	aaaatgaac	2639

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met	Lys	Asp	Met	Pro	Leu	Arg	Ile	His	Val	Leu	Leu	Gly	Leu	Ala	Ile	
1				5					10					15		
Thr	Thr	Leu	Val	Gln	Ala	Val	Asp	Lys	Lys	Val	Asp	Cys	Pro	Arg	Leu	
			20					25					30			
Cys	Thr	Cys	Glu	Ile	Arg	Pro	Trp	Phe	Thr	Pro	Arg	Ser	Ile	Tyr	Met	
		35					40					45				
Glu	Ala	Ser	Thr	Val	Asp	Cys	Asn	Asp	Leu	Gly	Leu	Leu	Thr	Phe	Pro	
	50					55					60					
Ala	Arg	Leu	Pro	Ala	Asn	Thr	Gln	Ile	Leu	Leu	Leu	Gln	Thr	Asn	Asn	
65					70					75					80	
Ile	Ala	Lys	Ile	Glu	Tyr	Ser	Thr	Asp	Phe	Pro	Val	Asn	Leu	Thr	Gly	
				85					90						95	
Leu	Asp	Leu	Ser	Gln	Asn	Asn	Leu	Ser	Ser	Val	Thr	Asn	Ile	Asn	Val	
			100					105					110			
Lys	Lys	Met	Pro	Gln	Leu	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Asn	Lys	Leu	
		115					120					125				
Thr	Glu	Leu	Pro	Glu	Lys	Cys	Leu	Ser	Glu	Leu	Ser	Asn	Leu	Gln	Glu	
	130					135					140					
Leu	Tyr	Ile	Asn	His	Asn	Leu	Leu	Ser	Thr	Ile	Ser	Pro	Gly	Ala	Phe	
145					150					155					160	
Ile	Gly	Leu	His	Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Arg	Leu	
				165					170					175		
Gln	Met	Ile	Asn	Ser	Lys	Trp	Phe	Asp	Ala	Leu	Pro	Asn	Leu	Glu	Ile	
			180					185					190			
Leu	Met	Ile	Gly	Glu	Asn	Pro	Ile	Ile	Arg	Ile	Lys	Asp	Met	Asn	Phe	
	195						200					205				
Lys	Pro	Leu	Ile	Asn	Leu	Arg	Ser	Leu	Val	Ile	Ala	Gly	Ile	Asn	Leu	
	210					215					220					
Thr	Glu	Ile	Pro	Asp	Asn	Ala	Leu	Val	Gly	Leu	Glu	Asn	Leu	Glu	Ser	
225					230					235					240	
Ile	Ser	Phe	Tyr	Asp	Asn	Arg	Leu	Ile	Lys	Val	Pro	His	Val	Ala	Leu	
				245					250					255		
Gln	Lys	Val	Val	Asn	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	Asn	Pro	Ile	
			260					265					270			
Asn	Arg	Ile	Arg	Arg	Gly	Asp	Phe	Ser	Asn	Met	Leu	His	Leu	Lys	Glu	

275					280					285					
Leu	Gly	Ile	Asn	Asn	Met	Pro	Glu	Leu	Ile	Ser	Ile	Asp	Ser	Leu	Ala
290						295					300				
Val	Asp	Asn	Leu	Pro	Asp	Leu	Arg	Lys	Ile	Glu	Ala	Thr	Asn	Asn	Pro
305					310					315					320
Arg	Leu	Ser	Tyr	Ile	His	Pro	Asn	Ala	Phe	Phe	Arg	Leu	Pro	Lys	Leu
				325					330					335	
Glu	Ser	Leu	Met	Leu	Asn	Ser	Asn	Ala	Leu	Ser	Ala	Leu	Tyr	His	Gly
			340					345					350		
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn
		355					360					365			
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
	370					375					380				
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro
385					390					395					400
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
				405					410					415	
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu
			420					425					430		
Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala
		435					440					445			
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu
	450					455					460				
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
465					470					475					480
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys
				485					490					495	
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys
			500					505					510		
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys
	515						520					525			
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser
	530					535					540				
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr
545					550					555					560
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys
				565					570					575	
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys

580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620
Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile		
625	630	635
Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp		
	645	650
Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala		
	660	665
		670
Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys		
	675	680
		685
Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro		
690	695	700
Thr Asn Met Ser		
705		

<210> 70
 <211> 1305
 <212> DNA
 <213> Homo sapiens

<400> 70

gcccgggact	ggcgcaaggt	gccaagcaa	ggaaagaaat	aatgaagaga	cacatgtgtt	60
agctgcagcc	ttttgaaaca	cgcaagaagg	aatcaatag	tgtggacagg	gctggaacct	120
ttaccacgct	tggtggagta	gatgaggaat	gggctcgtga	ttatgctgac	attccagcat	180
gaatctggta	gacctgtggt	taacccgttc	cctctccatg	tgtctcctcc	tacaaagttt	240
tgttcttatg	atactgtgct	ttcattctgc	cagtatgtgt	ccaaggggt	gtctttgttc	300
ttcctctggg	ggtttaaatg	tcacctgtag	caatgc aaa	ctcaaggaaa	tacctagaga	360
tcttcctcct	gaaacagtct	tactgtatct	ggactccaat	cagatcacat	ctattcccaa	420
tgaaattttt	aaggacctcc	atcaactgag	agttctcaac	ctgtccaaaa	atggcattga	480
gtttatcgat	gagcatgcct	tcaaaggagt	agctgaaacc	ttgcagactc	tggaactgtc	540
cgacaatcgg	attcaaagtg	tgcaaaaaaa	tgcttcaat	aacctgaagg	ccagggccag	600
aattgccaac	aacctctggc	actgcgactg	tactctacag	caagttctga	ggagcatggc	660
gtccaatcat	gagacagccc	acaacgtgat	ctgtaaaacg	tccgtgttgg	atgaacatgc	720
tggcagacca	ttcctcaatg	ctgccaacga	cgctgacctt	tgtaacctcc	ctaaaaaaac	780
taccgattat	gccatgctgg	tcaccatggt	tggctgggtc	actatgggtg	tctcatatgt	840
ggtatattat	gtgaggcaaa	atcaggagga	tgcccggaga	cacctcgaat	acttgaaatc	900
cctgccaagc	aggcagaaga	aagcagatga	acctgatgat	attagcactg	tggtatagtg	960
tccaaactga	ctgtcattga	gaaagaaaga	aagtagtttg	cgattgcagt	agaaataagt	1020
ggtttacttc	tcccatccat	tgtaaacatt	tgaaactttg	tatttcagtt	ttttttgaat	1080
tatgccactg	ctgaactttt	aacaaacact	acaacataaa	taatttgagt	ttaggtgatc	1140
caccctttaa	ttgtaccccc	gatggtatat	ttctgagtaa	gctactatct	gaacattagt	1200
tagatccatc	tcactattta	ataatgaaat	ttattttttt	aattttaaag	caaataaaag	1260
cttaactttg	aacctgggga	aaaaaaaaaa	aaaaaaaaaa	aaaca		1305

<210> 71
 <211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met	Asn	Leu	Val	Asp	Leu	Trp	Leu	Thr	Arg	Ser	Leu	Ser	Met	Cys	Leu	
1				5					10					15		
Leu	Leu	Gln	Ser	Phe	Val	Leu	Met	Ile	Leu	Cys	Phe	His	Ser	Ala	Ser	
			20					25					30			
Met	Cys	Pro	Lys	Gly	Cys	Leu	Cys	Ser	Ser	Ser	Gly	Gly	Leu	Asn	Val	
		35					40					45				
Thr	Cys	Ser	Asn	Ala	Asn	Leu	Lys	Glu	Ile	Pro	Arg	Asp	Leu	Pro	Pro	
	50					55					60					
Glu	Thr	Val	Leu	Leu	Tyr	Leu	Asp	Ser	Asn	Gln	Ile	Thr	Ser	Ile	Pro	
65					70					75					80	
Asn	Glu	Ile	Phe	Lys	Asp	Leu	His	Gln	Leu	Arg	Val	Leu	Asn	Leu	Ser	
				85					90					95		
Lys	Asn	Gly	Ile	Glu	Phe	Ile	Asp	Glu	His	Ala	Phe	Lys	Gly	Val	Ala	
			100					105					110			
Glu	Thr	Leu	Gln	Thr	Leu	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Gln	Ser	Val	
		115					120					125				
His	Lys	Asn	Ala	Phe	Asn	Asn	Leu	Lys	Ala	Arg	Ala	Arg	Ile	Ala	Asn	
	130					135					140					
Asn	Pro	Trp	His	Cys	Asp	Cys	Thr	Leu	Gln	Gln	Val	Leu	Arg	Ser	Met	
145					150					155					160	
Ala	Ser	Asn	His	Glu	Thr	Ala	His	Asn	Val	Ile	Cys	Lys	Thr	Ser	Val	
				165					170					175		
Leu	Asp	Glu	His	Ala	Gly	Arg	Pro	Phe	Leu	Asn	Ala	Ala	Asn	Asp	Ala	
			180					185					190			
Asp	Leu	Cys	Asn	Leu	Pro	Lys	Lys	Thr	Thr	Asp	Tyr	Ala	Met	Leu	Val	
		195					200					205				
Thr	Met	Phe	Gly	Trp	Phe	Thr	Met	Val	Ile	Ser	Tyr	Val	Val	Tyr	Tyr	
	210					215					220					
Val	Arg	Gln	Asn	Gln	Glu	Asp	Ala	Arg	Arg	His	Leu	Glu	Tyr	Leu	Lys	
225					230					235					240	
Ser	Leu	Pro	Ser	Arg	Gln	Lys	Lys	Ala	Asp	Glu	Pro	Asp	Asp	Ile	Ser	
				245					250					255		
Thr	Val	Val														

<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

```
accgagccga gcggaaccgaa ggcgcgcccc agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtag gagcatgccc agccccctcc tggcctgctg gcagcccatc ctctgctgg 120
tgctgggctc agtgctgtca ggctcggcca cgggctgccc gccccgctgc gactgctccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgctttgt ggagtcctcc gagggcatcc 240
ccaccgagac ggcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tggagccccg cgcttcaac aacctcttca acctccggac gctgggtctc cgagcaacc 420
gcctgaagct catcccgcga ggctcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcgtt atcctactgg actacatgtt tcaggacctg tacaacctca 540
agtcactgga ggttggcgac aatgacctcg tctacatctc tcaccgccc ttcagcgggc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgctc tgaggctccg gcacctcaac atcaatgcca 720
tccgggacta ctcttcaag aggctgtacc gactcaaggt cttggagatc tccactggc 780
ctactttgga caccatgaca cccaactgct tctacggcct caacctgacg tccctgtcca 840
tccacactg caactgtgac gctgtgcctt acctggcgt cgcgccaccta gtctatctcc 900
gcttcctcaa cctctcctac aacccccatca gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctgggtg gcgggcagct ggccgtgggtg gagccctatg 1020
ccttcgcgg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tggaggaatc agtcttccac tcgggtggga acctggagac actcatcctg gactccaacc 1140
cgctggcctg cgactgtcgg ctctgtggg tgttcggcg ccgctggcg ctcaacttca 1200
accggcagca gccacgtgc gccacggcg agtttgtcca gggcaaggag ttcaaggact 1260
tccctgatgt gctactgcc aactacttca cctgccgcg cgcccgcatc cgggaccgca 1320
aggcccagca ggtgtttgtg gacgagggc acacggtgca gtttgtgtgc cgggccgatg 1380
gcgaccggc gcccgccatc ctctggctct caccgccaaa gcacctggtc tcagccaaga 1440
gcaatggcg gctcacagtc ttccctgatg gcacgctgga ggtgcgtac gccaggtac 1500
aggacaacgg cagctacctg tgcctcgcg ccaacgcggg cggcaacgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactcgccc actggcccca tcagcccaac aagaccttcg 1620
ctttcatctc caaccagccg ggcgagggag aggcccaacag caccgcgcc actgtgcctt 1680
tccccttcga catcaagacc ctcatcatcg ccaccacat gggcttcatc tctttcctgg 1740
gcgtcgtcct ctctgcctg gtgctgctgt ttctctggag ccggggcaag ggcaacacaa 1800
agcacaacat cgagatcgag tatgtcccc gaaagtcgga cgcaggcatc agtccgccc 1860
acgcgcccc caagttaac atgaagatga tatgagccg gggcgggggg cagggacccc 1920
cggggcgccc ggcaggggaa ggggcctggt cgccacctgc tcaacttcca gtcttccca 1980
cctctcctc acccttctac acacgttctc tttctcctc cgcctccgt cccctgtgc 2040
cccccgccag cctcaccac ctgccctcct tctaccagga cctcagaagc ccagacctgg 2100
ggaccccacc tacacagggg cattgacaga ctggagtga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaa 2290
```

<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

```
Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
  1              5              10              15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
      20              25              30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
```

35					40					45					
Ser	Ala	Gln	Asp	Arg	Ala	Val	Leu	Cys	His	Arg	Lys	Cys	Phe	Val	Ala
50					55					60					
Val	Pro	Glu	Gly	Ile	Pro	Thr	Glu	Thr	Arg	Leu	Leu	Asp	Leu	Gly	Lys
65					70					75					80
Asn	Arg	Ile	Lys	Thr	Leu	Asn	Gln	Asp	Glu	Phe	Ala	Ser	Phe	Pro	His
				85					90					95	
Leu	Glu	Glu	Leu	Glu	Leu	Asn	Glu	Asn	Ile	Val	Ser	Ala	Val	Glu	Pro
			100					105					110		
Gly	Ala	Phe	Asn	Asn	Leu	Phe	Asn	Leu	Arg	Thr	Leu	Gly	Leu	Arg	Ser
		115					120					125			
Asn	Arg	Leu	Lys	Leu	Ile	Pro	Leu	Gly	Val	Phe	Thr	Gly	Leu	Ser	Asn
						135					140				
Leu	Thr	Lys	Gln	Asp	Ile	Ser	Glu	Asn	Lys	Ile	Val	Ile	Leu	Leu	Asp
145					150					155					160
Tyr	Met	Phe	Gln	Asp	Leu	Tyr	Asn	Leu	Lys	Ser	Leu	Glu	Val	Gly	Asp
				165					170					175	
Asn	Asp	Leu	Val	Tyr	Ile	Ser	His	Arg	Ala	Phe	Ser	Gly	Leu	Asn	Ser
			180					185					190		
Leu	Glu	Gln	Leu	Thr	Leu	Glu	Lys	Cys	Asn	Leu	Thr	Ser	Ile	Pro	Thr
			195					200					205		
Glu	Ala	Leu	Ser	His	Leu	His	Gly	Leu	Ile	Val	Leu	Arg	Leu	Arg	His
						215					220				
Leu	Asn	Ile	Asn	Ala	Ile	Arg	Asp	Tyr	Ser	Phe	Lys	Arg	Leu	Tyr	Arg
225						230					235				240
Leu	Lys	Val	Leu	Glu	Ile	Ser	His	Trp	Pro	Tyr	Leu	Asp	Thr	Met	Thr
				245					250					255	
Pro	Asn	Cys	Leu	Tyr	Gly	Leu	Asn	Leu	Thr	Ser	Leu	Ser	Ile	Thr	His
			260					265					270		
Cys	Asn	Leu	Thr	Ala	Val	Pro	Tyr	Leu	Ala	Val	Arg	His	Leu	Val	Tyr
			275				280					285			
Leu	Arg	Phe	Leu	Asn	Leu	Ser	Tyr	Asn	Pro	Ile	Ser	Thr	Ile	Glu	Gly
						295					300				
Ser	Met	Leu	His	Glu	Leu	Leu	Arg	Leu	Gln	Glu	Ile	Gln	Leu	Val	Gly
305						310					315				320
Gly	Gln	Leu	Ala	Val	Val	Glu	Pro	Tyr	Ala	Phe	Arg	Gly	Leu	Asn	Tyr
				325					330					335	
Leu	Arg	Val	Leu	Asn	Val	Ser	Gly	Asn	Gln	Leu	Thr	Thr	Leu	Glu	Glu

340					345					350					
Ser	Val	Phe	His	Ser	Val	Gly	Asn	Leu	Glu	Thr	Leu	Ile	Leu	Asp	Ser
		355					360					365			
Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Val	Phe	Arg	Arg	Arg
		370					375					380			
Trp	Arg	Leu	Asn	Phe	Asn	Arg	Gln	Gln	Pro	Thr	Cys	Ala	Thr	Pro	Glu
		385					390					395			400
Phe	Val	Gln	Gly	Lys	Glu	Phe	Lys	Asp	Phe	Pro	Asp	Val	Leu	Leu	Pro
				405					410					415	
Asn	Tyr	Phe	Thr	Cys	Arg	Arg	Ala	Arg	Ile	Arg	Asp	Arg	Lys	Ala	Gln
			420					425					430		
Gln	Val	Phe	Val	Asp	Glu	Gly	His	Thr	Val	Gln	Phe	Val	Cys	Arg	Ala
		435					440					445			
Asp	Gly	Asp	Pro	Pro	Pro	Ala	Ile	Leu	Trp	Leu	Ser	Pro	Arg	Lys	His
		450					455					460			
Leu	Val	Ser	Ala	Lys	Ser	Asn	Gly	Arg	Leu	Thr	Val	Phe	Pro	Asp	Gly
				470								475			480
Thr	Leu	Glu	Val	Arg	Tyr	Ala	Gln	Val	Gln	Asp	Asn	Gly	Thr	Tyr	Leu
				485					490					495	
Cys	Ile	Ala	Ala	Asn	Ala	Gly	Gly	Asn	Asp	Ser	Met	Pro	Ala	His	Leu
			500					505					510		
His	Val	Arg	Ser	Tyr	Ser	Pro	Asp	Trp	Pro	His	Gln	Pro	Asn	Lys	Thr
		515					520					525			
Phe	Ala	Phe	Ile	Ser	Asn	Gln	Pro	Gly	Glu	Gly	Glu	Ala	Asn	Ser	Thr
		530					535					540			
Arg	Ala	Thr	Val	Pro	Phe	Pro	Phe	Asp	Ile	Lys	Thr	Leu	Ile	Ile	Ala
				550					555						560
Thr	Thr	Met	Gly	Phe	Ile	Ser	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Leu
				565					570					575	
Val	Leu	Leu	Phe	Leu	Trp	Ser	Arg	Gly	Lys	Gly	Asn	Thr	Lys	His	Asn
			580					585					590		
Ile	Glu	Ile	Glu	Tyr	Val	Pro	Arg	Lys	Ser	Asp	Ala	Gly	Ile	Ser	Ser
		595					600					605			
Ala	Asp	Ala	Pro	Arg	Lys	Phe	Asn	Met	Lys	Met	Ile				
		610					615				620				

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 74
 tcacctggag cctttattgg cc 22

<210> 75
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 75
 ataccagcta taaccaggct gcg 23

<210> 76
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 76
 caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg 50
 gg 52

<210> 77
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 77
 ccatgtgtct cctcctacaa ag 22

<210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 78
 gggaatagat gtgatctgat tgg 23

<210> 79
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 79
 cacctgtagc aatgcaaadc tcaaggaaat acctagagat cttcctcctg 50

 <210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 80
 agcaaccgcc tgaagctcat cc 22

 <210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 81
 aaggcgcggt gaaagatgta gacg 24

 <210> 82
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 82
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

 <210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

 <400> 83
 cccacgcgtc cgcacctcgg ccccgaggctc cgaagcggct cggggggcgcc ctttcgggtca 60
 acatcgtagt ccacccctc cccatcccca gccccgggg attcaggctc gccagcgccc 120
 agccaggag cgggcccggga agcgcgatgg gggccccagc cgctcgcgtc ctgctcctgc 180

```

tcctgctgtt cgccctgctgc tgggcgcccc gcgggggccaa cctctcccag gacgacagcc 240
agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtgccaa 300
tgaaagatca cgaggactca tccctgcaat ggtctaacc tgctcagcag actctctact 360
ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420
agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480
tcttcactat gcctgtgcga actgccaagt cctcgtcac tgtgctagga attccacaga 540
agcccatcat cactgggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600
gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggg gaccaagaac 660
tccacggaga accaaccgcg atacaggaag atcccaatgg taaaaccttc actgtcagca 720
gctcggtgac attccagggt acccgggagg atgatggggc gagcatcgtg tgctctgtga 780
accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gttttataca 840
caccaactgc gatgattagg ccagaccctc cccatcctcg tgagggccag aagctgttgc 900
tacactgtga gggtcgcggc aatccagtcc cccagcagta cctatgggag aaggagggca 960
gtgtgccacc cctgaagatg acccaggaga gtgccctgat ctcccttttc ctcaacaaga 1020
gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080
acaccctcaa tgtaaatgac cccagtccgg tgccctctc ctccagcacc taccacgcca 1140
tcatcgggtg gatcgtggct ttcattgtct tctgctgct catcatgctc atcttcttg 1200
gccactactt gatccggcac aaaggaacct acctgacaca tgaggcaaaa ggctccgacg 1260
atgctccaga cgcggacag gccatcatca atgcagaagg cgggcagtca ggaggggacg 1320
acaagaagga atatttcac tagaggcgc tgcaccttc ctgcgcccc caggggccct 1380
gtggggactg ctggggccgt caccaaccgc gactgtaca gagcaaccgc agggccgccc 1440
ctcccgcttg ctccccagcc caccacccc cctgtacaga atgtctgctt tgggtgcggt 1500
tttgtactcg gtttggaatg gggagggagg agggcgggg gaggggaggg ttgccctcag 1560
ccctttccgt ggcttctctg catttggtt attattatt ttgtaacaat cccaaatcaa 1620
atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaacaaa 1680
aaaca
1685

```

<210> 84

<211> 398

<212> PRT

<213> Homo sapiens

<400> 84

```

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
  1              5              10              15

Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
      20              25              30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
  35              40              45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
  50              55              60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
  65              70              75              80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
      85              90              95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
      100             105             110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
      115             120             125

```

Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu	130	135	140
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala	145	150	155
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro	165	170	175
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser	180	185	190
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val	195	200	205
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser	210	215	220
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp	225	230	235
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly	245	250	255
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser	260	265	270
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe	275	280	285
Leu	Asn	Lys	Ser	Asp	Ser	Gly	Thr	Tyr	Gly	Cys	Thr	Ala	Thr	Ser	Asn	290	295	300
Met	Gly	Ser	Tyr	Lys	Ala	Tyr	Tyr	Thr	Leu	Asn	Val	Asn	Asp	Pro	Ser	305	310	315
Pro	Val	Pro	Ser	Ser	Ser	Ser	Thr	Tyr	His	Ala	Ile	Ile	Gly	Gly	Ile	325	330	335
Val	Ala	Phe	Ile	Val	Phe	Leu	Leu	Leu	Ile	Met	Leu	Ile	Phe	Leu	Gly	340	345	350
His	Tyr	Leu	Ile	Arg	His	Lys	Gly	Thr	Tyr	Leu	Thr	His	Glu	Ala	Lys	355	360	365
Gly	Ser	Asp	Asp	Ala	Pro	Asp	Ala	Asp	Thr	Ala	Ile	Ile	Asn	Ala	Glu	370	375	380
Gly	Gly	Gln	Ser	Gly	Gly	Asp	Asp	Lys	Lys	Glu	Tyr	Phe	Ile			385	390	395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 87

cctagcacag tgacgagga cttggc

26

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 88

aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc

50

<210> 89

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 89

gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt

50

<210> 90

<211> 2755

<212> DNA

<213> Homo sapiens

<400> 90

gggggttagg	gaggaaggaa	tccaccccc	ccccccaaa	cccttttctt	ctcctttcct	60
ggcttcggac	attggagcac	taaatgaact	tgaattgtgt	ctgtggcgag	caggatgggc	120
gctgttactt	tgtgatgaga	tcggggatga	attgctcgct	ttaaaaatgc	tgctttggat	180
tctgttgctg	gagacgtctc	tttgttttgc	cgctggaaac	gttacagggg	acgtttgcaa	240
agagaagatc	tgttcctgca	atgagataga	aggggaccta	cacgtagact	gtgaaaaaaa	300
gggcttcaca	agtctgcagc	gtttcactgc	cccgaacttc	cagttttacc	atatttttct	360
gcatggcaat	tccctcactc	gacttttccc	taatgagttc	gctaactttt	ataatgcggt	420
tagtttgcac	atggaaaaca	atggcttgca	tgaatcggtt	ccgggggctt	ttctggggct	480
gcagctgggtg	aaaaggctgc	acatcaacaa	caacaagatc	aagtcttttc	gaaagcagac	540
ttttctgggg	ctggacgatc	tgggaatatc	ccaggctgat	tttaatttat	tacgagatat	600
agaccggggg	gccttcagg	acttgaacaa	gctggagggtg	ctcattttta	atgacaatct	660
catcagcacc	ctacctgcca	acgtgttcca	gtatgtgccc	atcaccacc	tcgacctccg	720
gggtaacagg	ctgaaaacgc	tgccctatga	ggaggctctg	gagcaaatac	ctggtattgc	780
ggagatcctg	ctagaggata	acccttgga	ctgcacctgt	gatctgctct	ccctgaaaga	840
atggctggaa	aacattccca	agaatgccct	gatcggccga	gtggtctgcg	aagccccac	900
cagactgcag	ggtaaagacc	tcaatgaaac	caccgaacag	gacttgtgtc	ctttgaaaaa	960
ccgagtggat	tctatgtccc	cggcgccccc	tgcccaagaa	gagacctttg	ctcctggacc	1020
cctgccaaact	cttttcaaga	caaattggga	agaggatcat	gccacaccag	gggtctgctcc	1080
aaacggagggt	acaaagatcc	caggcaactg	gcagatcaaa	atcagaccca	cagcagcgat	1140
agcgacgggt	agctccagga	acaaaccctt	agctaacagt	ttaccctgcc	ctgggggctg	1200
cagctgcgac	cacatcccag	ggtcgggttt	aaagatgaac	tgcaacaaca	ggaacgtgag	1260
cagcttggtc	gatttgaagc	ccaagctctc	taacgtgcag	gagcttttcc	tacgagataa	1320
caagatccac	agcatccgaa	aatcgcaact	tgtggattac	aagaacctca	ttctgttgga	1380
tctgggcaac	aataacatcg	ctactgtaga	gaacaacact	ttcaagaacc	ttttggacct	1440
caggtggcta	tacatggata	gcaattacct	ggacacgctg	ttccgggaga	aattcgcggg	1500
gctgcaaaac	ctagagtacc	tgaacgtgga	gtacaacgct	atccagctca	tcctcccggg	1560
cactttcaat	gccatgccc	aactgaggat	cctcattctc	aacaacaacc	tgctgagggtc	1620
cctgcctgtg	gacgtgttcg	ctgggggtctc	gctctctaaa	ctcagcctgc	acaacaatta	1680
cttcatgtac	ctcccgggtg	caggggtgct	ggaccagtta	acctccatca	tccagataga	1740
cctccacgga	aacccttggg	agtgtcctctg	cacaattgtg	cctttcaagc	agtgggcaga	1800
acgcttgggt	tccgaagtgc	tgatgagcga	cctcaagtgt	gagacgccgg	tgaacttctt	1860
tagaaaggat	ttcatgtctc	tctccaatga	cgagatctgc	cctcagctgt	acgctaggat	1920
ctcgcccacg	ttactttcgc	acagtaaaaa	cagcactggg	ttggcggaga	ccgggacgca	1980
ctccaactcc	tacctagaca	ccagcagggt	gtccatctcg	gtgttggtcc	cgggactgct	2040
gctggtgttt	gtcacctccg	ccttcaccgt	gggtggcag	ctcgtgttta	tcctgaggaa	2100
ccgaaagcgg	tccaagagac	gagatgccaa	ctcctccg	tccgagatta	attccctaca	2160
gcagctgtgt	gactcttccc	actggcaca	tgggccttac	aacgcagatg	gggcccacag	2220
agtgtatgac	tgtggctctc	actcgctctc	agactaagac	cccaacccca	ataggggagg	2280
gcagagggaa	ggcgatacat	ccttccccac	cgcaggcacc	ccgggggctg	gaggggctg	2340
tacccaaatc	ccgcgccat	cagcctggat	gggcataagt	agataaataa	ctgtgagctc	2400
gcacaaccga	aagggcctga	cccccttact	agctccctcc	ttgaaacaaa	gagcagactg	2460
tggagagctg	ggagagcgca	gccagctcgc	tctttgctga	gagccccctt	tgacagaaag	2520
cccagcacga	ccctgctgga	agaactgaca	gtgcctcgc	cctcgcccc	ggggcctgtg	2580
gggttggtatg	ccgcggttct	atacatatat	acatatatcc	acatctatat	agagagatag	2640
atatctattt	ttcccctgtg	gattagcccc	gtgatggctc	cctgttggtc	acgcagggat	2700
gggcagttgc	acgaaggcat	gaatgtattg	taaataagta	actttgactt	ctgac	2755

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala

1	5	10	15
Gly Asn Val Thr	Gly Asp Val Cys Lys	Glu Lys Ile Cys Ser	Cys Asn
20	25	30	
Glu Ile Glu Gly Asp	Leu His Val Asp Cys	Glu Lys Lys Gly Phe Thr	
35	40	45	
Ser Leu Gln Arg Phe Thr	Ala Pro Thr Ser Gln Phe Tyr	His Leu Phe	
50	55	60	
Leu His Gly Asn Ser	Leu Thr Arg Leu Phe Pro	Asn Glu Phe Ala Asn	
65	70	75	80
Phe Tyr Asn Ala Val	Ser Leu His Met Glu Asn	Asn Gly Leu His Glu	
85	90	95	
Ile Val Pro Gly Ala Phe	Leu Gly Leu Gln Leu Val Lys	Arg Leu His	
100	105	110	
Ile Asn Asn Asn Lys	Ile Lys Ser Phe Arg Lys	Gln Thr Phe Leu Gly	
115	120	125	
Leu Asp Asp Leu Glu Tyr	Leu Gln Ala Asp Phe Asn	Leu Leu Arg Asp	
130	135	140	
Ile Asp Pro Gly Ala Phe	Gln Asp Leu Asn Lys Leu Glu	Val Leu Ile	
145	150	155	160
Leu Asn Asp Asn Leu Ile	Ser Thr Leu Pro Ala Asn	Val Phe Gln Tyr	
165	170	175	
Val Pro Ile Thr His Leu	Asp Leu Arg Gly Asn Arg	Leu Lys Thr Leu	
180	185	190	
Pro Tyr Glu Glu Val Leu	Glu Gln Ile Pro Gly Ile	Ala Glu Ile Leu	
195	200	205	
Leu Glu Asp Asn Pro Trp	Asp Cys Thr Cys Asp	Leu Leu Ser Leu Lys	
210	215	220	
Glu Trp Leu Glu Asn Ile	Pro Lys Asn Ala Leu Ile	Gly Arg Val Val	
225	230	235	240
Cys Glu Ala Pro Thr	Arg Leu Gln Gly Lys Asp	Leu Asn Glu Thr Thr	
245	250	255	
Glu Gln Asp Leu Cys Pro	Leu Lys Asn Arg Val Asp	Ser Ser Leu Pro	
260	265	270	
Ala Pro Pro Ala Gln Glu	Glu Thr Phe Ala Pro Gly	Pro Leu Pro Thr	
275	280	285	
Pro Phe Lys Thr Asn Gly	Gln Glu Asp His Ala Thr	Pro Gly Ser Ala	
290	295	300	
Pro Asn Gly Gly Thr Lys	Ile Pro Gly Asn Trp Gln	Ile Lys Ile Arg	

305		310		315		320
Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala						
		325		330		335
Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly						
		340		345		350
Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala						
		355		360		365
Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp						
		370		375		380
Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn						
		385		390		400
Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn						
		405		410		415
Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser						
		420		425		430
Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn						
		435		440		445
Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro						
		450		455		460
Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn						
		465		470		475
Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu						
		485		490		495
Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala						
		500		505		510
Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly						
		515		520		525
Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala						
		530		535		540
Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr						
		545		550		555
Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu						
		565		570		575
Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His						
		580		585		590
Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser						
		595		600		605
Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu						

610	615	620
Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val		
625	630	635 640
Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser		
	645	650 655
Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr		
	660	665 670
Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp		
	675	680 685
Cys Gly Ser His Ser Leu Ser Asp		
	690	695

<210> 92
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 92
 gttggatctg ggcaacaata ac 22

<210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 93
 attgttgtgc aggctgagtt taag 24

<210> 94
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 94
 ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95
 <211> 2226
 <212> DNA
 <213> Homo sapiens

<400> 95

```
agtcgactgc gtccccctgta cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60
gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgcggcctaa gggaaactgt 120
tgcccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180
gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaatgaggc cggcgttcgc cctgtgcctc ctctggcagg cgctctggcc 360
cgggcccggg ggcggcgaac accccactgc cgaccgtgct ggctgctcgg cctcgggggg 420
ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcatacct 480
gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgctcgcgct 540
cctgcgggca ggcccagggc ccggaggggg ctccaaagac ctgctgttct gggtcgcact 600
ggagcgcagg cgttccact gcaccctgga gaacgagcct ttgcgggggt tctcctggct 660
gtcctccgac cccggcgggtc tcgaaagcga cacgctgcag tgggtggagg agccccaacg 720
ctcctgcacc gcgcggagat gcgcggtact ccaggccacc ggtggggctg agcccgcagg 780
ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840
ggtcttgtgt cctgcgccgc gcccgggggc cgctctaac ttgagctatc gcgcgccctt 900
ccagctgcac agcgcgcgtc tggacttcag tccacctggg accgaggtga gtgcgctctg 960
ccggggacag ctcccgatct cagttacttg catcgcggac gaaatcggcg ctgcgtggga 1020
caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacctccgtg ctggcaaattg 1080
cgcagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgctacggg 1140
cttcgagctg ggggaaggac gcgctcttg tgtgaccagt ggggaaggac agccgaccct 1200
tggggggacc ggggtgccc ccaggcgccc gccggccact gcaaccagcc ccgtgccgca 1260
gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320
agacaattca gtaacatcta ttcttgagat tctctgatgg ggatcacaga gcacgatgtc 1380
tacccttcaa atgtcccttc aagccgagtc aaaggccact atcacccat caggagcgt 1440
gatttccaag tttaattcta cgacttcctc tgccactcct caggctttcg actcctcctc 1500
tgccgtggtc ttcataattg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560
agtactgggg cttgtcaagc tctgctttca cgaaagcccc tcttcccagc caaggaagga 1620
gtctatgggc ccgccggggc tggagagtga tcctgagccc gctgctttgg gctccagttc 1680
tgcacattgc acaaacaatg gggtgaaagt cggggactgt gatctgcggg acagagcaga 1740
gggtgccttg ctggcggagt cccctcttgg ctctagtgat gcatagggaa acaggggaca 1800
tgggcactcc tgtgaacagt ttttacttt tgatgaaacg gggaaccaag aggaacttac 1860
ttgtgtaact gacaatttct gcagaaatcc ccttctctt aaattccctt tactccactg 1920
aggagctaaa tcagaactgc aactccttc cctgatgata gaggaagtgg aagtgccttt 1980
aggatggtga tactggggga ccgggtagt ctggggagag atattttctt atgtttattc 2040
ggagaatttg gagaagtgat tgaacttttc aagacattgg aaacaaatag aacacaatat 2100
aatttacatt aaaaaataat ttctacaaa atggaaaagg aatgttctat gttgttcagg 2160
ctaggagtat attggttcga aatcccaggg aaaaaataa aaataaaaaa ttaaaggatt 2220
gttgat 2226
```

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

```
Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
 1                      5                      10                      15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
                20                      25                      30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
          35                      40                      45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
```

50					55					60					
Arg	Ala	Gly	Ala	Glu	Leu	Arg	Ala	Val	Leu	Ala	Leu	Leu	Arg	Ala	Gly
65					70					75					80
Pro	Gly	Pro	Gly	Gly	Gly	Ser	Lys	Asp	Leu	Leu	Phe	Trp	Val	Ala	Leu
				85					90					95	
Glu	Arg	Arg	Arg	Ser	His	Cys	Thr	Leu	Glu	Asn	Glu	Pro	Leu	Arg	Gly
			100					105					110		
Phe	Ser	Trp	Leu	Ser	Ser	Asp	Pro	Gly	Gly	Leu	Glu	Ser	Asp	Thr	Leu
		115					120					125			
Gln	Trp	Val	Glu	Glu	Pro	Gln	Arg	Ser	Cys	Thr	Ala	Arg	Arg	Cys	Ala
		130					135				140				
Val	Leu	Gln	Ala	Thr	Gly	Gly	Val	Glu	Pro	Ala	Gly	Trp	Lys	Glu	Met
145					150					155					160
Arg	Cys	His	Leu	Arg	Ala	Asn	Gly	Tyr	Leu	Cys	Lys	Tyr	Gln	Phe	Glu
			165						170					175	
Val	Leu	Cys	Pro	Ala	Pro	Arg	Pro	Gly	Ala	Ala	Ser	Asn	Leu	Ser	Tyr
			180					185					190		
Arg	Ala	Pro	Phe	Gln	Leu	His	Ser	Ala	Ala	Leu	Asp	Phe	Ser	Pro	Pro
		195					200					205			
Gly	Thr	Glu	Val	Ser	Ala	Leu	Cys	Arg	Gly	Gln	Leu	Pro	Ile	Ser	Val
	210						215					220			
Thr	Cys	Ile	Ala	Asp	Glu	Ile	Gly	Ala	Arg	Trp	Asp	Lys	Leu	Ser	Gly
225					230					235					240
Asp	Val	Leu	Cys	Pro	Cys	Pro	Gly	Arg	Tyr	Leu	Arg	Ala	Gly	Lys	Cys
				245					250					255	
Ala	Glu	Leu	Pro	Asn	Cys	Leu	Asp	Asp	Leu	Gly	Gly	Phe	Ala	Cys	Glu
			260					265					270		
Cys	Ala	Thr	Gly	Phe	Glu	Leu	Gly	Lys	Asp	Gly	Arg	Ser	Cys	Val	Thr
		275					280					285			
Ser	Gly	Glu	Gly	Gln	Pro	Thr	Leu	Gly	Gly	Thr	Gly	Val	Pro	Thr	Arg
	290					295					300				
Arg	Pro	Pro	Ala	Thr	Ala	Thr	Ser	Pro	Val	Pro	Gln	Arg	Thr	Trp	Pro
305					310					315					320
Ile	Arg	Val	Asp	Glu	Lys	Leu	Gly	Glu	Thr	Pro	Leu	Val	Pro	Glu	Gln
			325						330					335	
Asp	Asn	Ser	Val	Thr	Ser	Ile	Pro	Glu	Ile	Pro	Arg	Trp	Gly	Ser	Gln
			340					345					350		
Ser	Thr	Met	Ser	Thr	Leu	Gln	Met	Ser	Leu	Gln	Ala	Glu	Ser	Lys	Ala

355					360					365						
Thr	Ile	Thr	Pro	Ser	Gly	Ser	Val	Ile	Ser	Lys	Phe	Asn	Ser	Thr	Thr	
370					375					380						
Ser	Ser	Ala	Thr	Pro	Gln	Ala	Phe	Asp	Ser	Ser	Ser	Ala	Val	Val	Phe	
385					390					395					400	
Ile	Phe	Val	Ser	Thr	Ala	Val	Val	Val	Leu	Val	Ile	Leu	Thr	Met	Thr	
					405					410					415	
Val	Leu	Gly	Leu	Val	Lys	Leu	Cys	Phe	His	Glu	Ser	Pro	Ser	Ser	Gln	
					420					425					430	
Pro	Arg	Lys	Glu	Ser	Met	Gly	Pro	Pro	Gly	Leu	Glu	Ser	Asp	Pro	Glu	
					435					440					445	
Pro	Ala	Ala	Leu	Gly	Ser	Ser	Ser	Ala	His	Cys	Thr	Asn	Asn	Gly	Val	
					450					455					460	
Lys	Val	Gly	Asp	Cys	Asp	Leu	Arg	Asp	Arg	Ala	Glu	Gly	Ala	Leu	Leu	
465					470					475					480	
Ala	Glu	Ser	Pro	Leu	Gly	Ser	Ser	Asp	Ala							
					485					490						

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 97

tggaaggaga tgcgatgcca cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20

<210> 99

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 99

acagagcaga ggggtgccttg

20

<210> 100

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 100

tcagggacaa gtggtgtctc tccc

24

<210> 101

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 101

tcagggaagg agtgtgcagt tctg

24

<210> 102

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 102

acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct

50

<210> 103

<211> 2026

<212> DNA

<213> Homo sapiens

<400> 103

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120
tatcccccg ctacctgggc cgccccgcgc cggtgcgcgc gtgagaggga gcgcgcgggc 180
agccgagcgc cggtgtgagc cagcgcgtgt gccagtgtga gcggcgggtg gagcgcgggtg 240
ggtgcggagg ggcggtgtgt ccggcgcgcgc cgccgtgggg tgcaaaccac gagcgtctac 300
gctgccatga ggggcgcgaa cgccctgggc ccactctgcc tgctgctggc tgccgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gatttatttg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttga aaatcacagt tcccgaagga aaagtagtcg ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600

```

aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
ggcaacaaga tgatggtgca gatgatttct gatgccaaca cagctggcaa tggcttcatg 720
gccatgttct ccgctgctga accaaacgaa agaggggatc agtattgtgg aggactcctt 780
gacagacctt ccggctcttt taaaaccccc aactggccag accgggatta ccctgcagga 840
gtcacttgtg tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900
aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaatggc 960
ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtcc acctgcgcca 1020
attgtgtctg agagaaatga acttcttatt cagtttttat cagacttaag tttaactgca 1080
gatgggttta ttggtcacta catattcagg ccaaaaaaac tgcctacaac tacagaacag 1140
cctgtcacca ccacattccc tgtaaccacg ggtttaaaac ccaccgtggc cttgtgtcaa 1200
caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
gccggcactg ttatcacaaac catcactcgc gatgggagtt tgcacgccac agtctcgatc 1320
atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380
aggctgactg tcgtctgcaa gcagtgcctt ctctcagaa gaggtctaaa ttacattatt 1440
atgggccaa taggtgaaga tgggcgaggc aaaatcatgc caaacagctt tatcatgatg 1500
ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560
actgtgtcca tttaagctgt attctgccat tgcctttgaa agatctatgt tctctcagta 1620
gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggagtg 1680
ttgactcttc acatgatgga ggtatgaggc tcccgagata gctgagggaa gttctttgcc 1740
tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800
ctaaaagtgt caagcgttga cagcttggaa gcgtttatct atacatctct gtaaaaggat 1860
attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
gtgttatattg ttccaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

<210> 104
 <211> 415
 <212> PRT
 <213> Homo sapiens

```

<400> 104
Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1              5              10              15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20              25              30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35              40              45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50              55              60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
      65              70              75              80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
      85              90              95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
      100              105              110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
      115              120              125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
      130              135              140

```

Glu	Pro	Asn	Glu	Arg	Gly	Asp	Gln	Tyr	Cys	Gly	Gly	Leu	Leu	Asp	Arg	
145					150					155					160	
Pro	Ser	Gly	Ser	Phe	Lys	Thr	Pro	Asn	Trp	Pro	Asp	Arg	Asp	Tyr	Pro	
				165					170					175		
Ala	Gly	Val	Thr	Cys	Val	Trp	His	Ile	Val	Ala	Pro	Lys	Asn	Gln	Leu	
			180					185					190			
Ile	Glu	Leu	Lys	Phe	Glu	Lys	Phe	Asp	Val	Glu	Arg	Asp	Asn	Tyr	Cys	
		195					200					205				
Arg	Tyr	Asp	Tyr	Val	Ala	Val	Phe	Asn	Gly	Gly	Glu	Val	Asn	Asp	Ala	
	210					215					220					
Arg	Arg	Ile	Gly	Lys	Tyr	Cys	Gly	Asp	Ser	Pro	Pro	Ala	Pro	Ile	Val	
225					230					235					240	
Ser	Glu	Arg	Asn	Glu	Leu	Leu	Ile	Gln	Phe	Leu	Ser	Asp	Leu	Ser	Leu	
			245						250					255		
Thr	Ala	Asp	Gly	Phe	Ile	Gly	His	Tyr	Ile	Phe	Arg	Pro	Lys	Lys	Leu	
		260						265					270			
Pro	Thr	Thr	Thr	Glu	Gln	Pro	Val	Thr	Thr	Thr	Phe	Pro	Val	Thr	Thr	
		275					280					285				
Gly	Leu	Lys	Pro	Thr	Val	Ala	Leu	Cys	Gln	Gln	Lys	Cys	Arg	Arg	Thr	
	290					295					300					
Gly	Thr	Leu	Glu	Gly	Asn	Tyr	Cys	Ser	Ser	Asp	Phe	Val	Leu	Ala	Gly	
305					310					315					320	
Thr	Val	Ile	Thr	Thr	Ile	Thr	Arg	Asp	Gly	Ser	Leu	His	Ala	Thr	Val	
				325					330					335		
Ser	Ile	Ile	Asn	Ile	Tyr	Lys	Glu	Gly	Asn	Leu	Ala	Ile	Gln	Gln	Ala	
			340					345					350			
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro	
		355					360					365				
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu	
		370				375					380					
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys	
385					390					395					400	
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys		
			405						410					415		

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105
ccgattcata gacctcgaga gt 22

<210> 106
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106
gtcaaggagt cctccacaat ac 22

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45

<210> 108
<211> 1838
<212> DNA
<213> Homo sapiens

<400> 108
cggacgcgtg ggcggacgcg tgggcgggccc acggcgcccc cggtcgcttc 60
ttccttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgctcagcc ccatccgtgt 240
catacctgcc ggggactggg tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaaacac tgctgggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggg gtgtgcagca agtcagactt cgagtgccac 420
cgcttctgtg agctgagtga ggagctgggt gagagctggg ggtttcacia gcagcaggag 480
gccccggacc tcttccagtg gctgtgctca gattccctga agctctgtg ccccgaggc 540
accttcgggc cctcctgcct tccctgtcct gggggaacag agaggccctg cgggtggctac 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
agccatctgg tatgttcggc ttgttttggc ccctgtgccc gatgctcagg acctgaggaa 780
tcaaactgtt tgcaatgcaa gaagggtctg gccctgcac acctcaagtg tgtagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaa gacctgcctag gctgcatggg ggcaggggcca 960
ggtcgctgta agaagtgtag ccttggtat cagcagggtg gctccaagtg tctcgatgtg 1020
gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080
ggttatcgct gcactctgtc cgagggtac aagcagatgg aaggcatctg tgtgaaggag 1140
cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200

```

cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taagggcgac 1260
ttggtgttca ccgccatctt cattggggct gtggcgcca tgactggcta ctggttgtca 1320
gagcgcagt accgtgtgct ggagggcttc atcaaggcca gataatcgcg gccaccacct 1380
gtaggacct ctcaccacca cgctgcccc agagcttggg ctgccctcct gctggacact 1440
caggacagct tggtttattt ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500
gccaggtac ccaggcccgg gcagacaagg cccctgggg aaaaagtagc cctgaagggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
agtttttcct taatggtggc tgctagagct ttggcccctg cttaggatta ggtggtcctc 1680
acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tcctgttctg 1740
tgttcaccac atccccacac cccattgcc aattttatt catctcagga aataaagaaa 1800
ggtcttgtaa agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

```

<210> 109
 <211> 420
 <212> PRT
 <213> Homo sapiens

<400> 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
 1              5              10              15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50              55              60

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
      65              70              75              80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
      85              90              95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
      100             105             110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
      115             120             125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
      130             135             140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
      145             150             155             160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
      165             170             175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
      180             185             190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
      195             200             205

```

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 210 215 220
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 225 230 235 240
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
 245 250 255
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 260 265 270
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 275 280 285
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 290 295 300
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 325 330 335
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350
 Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365
 Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380
 Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400
 Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415
 Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1461)..(1461)

<223> a, t, c or g

<400> 113

tgagaccctc	ctgcagcctt	ctcaagggac	agccccactc	tgcctcttgc	tcctccaggg	60
cagcaccatg	cagccccgtg	ggctctgctg	ggcactctgg	gtgttgcccc	tggccagccc	120
cggggccgcc	ctgaccgggg	agcagctcct	gggcagcctg	ctgcggcagc	tgcagctcaa	180
agaggtgccc	accctggaca	gggccgacat	ggaggagctg	gtcatcccca	cccacgtgag	240
ggcccagtag	gtggccctgc	tgcagcgcag	ccacggggac	cgctcccgcg	gaaagaggtt	300
cagccagagc	ttccgagagg	tggccggcag	gttcctggcg	ttggaggcca	gcacacacct	360
gctgggtgtt	ggcatggagc	agcggctgcc	gccccaacag	gagctgggtg	aggccgtgct	420
gcggctcttc	caggagccgg	tccccaaagg	cgcgctgcac	aggcacgggc	ggctgtcccc	480
gcgcagcgcc	cggggccggg	tgaccgtcga	gtggctgcgc	gtccgcgacg	acggctccaa	540
ccgcacctcc	ctcatcgact	ccaggctggg	gtccgtccac	gagagcggct	ggaaggcctt	600
cgacgtgacc	gaggccgtga	acttctggca	gcagctgagc	cggccccggc	agccgctgct	660
gctacaggtg	tcggtgcaga	gggagcatct	gggcccgtg	gcgtccggcg	cccacaagct	720
ggtccgcttt	gcctcgcagg	gggcgccagc	cgggcttggg	gagccccagc	tggagctgca	780
caccctggac	cttggggact	atggagctca	gggcgactgt	gaccctgaag	caccaatgac	840
cgagggcacc	cgctgctgcc	gccaggagat	gtacattgac	ctgcagggga	tgaagtgggc	900
cgagaactgg	gtgctggagc	ccccgggctt	cctggcttat	gagtgtgtgg	gcacctgccg	960
gcagcccccg	gaggccctgg	ccttcaagtg	gccgtttctg	gggcctcgac	agtgcctgcg	1020
ctcggagact	gactcgctgc	ccatgatcgt	cagcatcaag	gagggaggca	ggaccaggcc	1080
ccagggtggc	agcctgcccc	acatgagggg	gcagaagtgc	agctgtgcct	cggatgggtg	1140
gctcgtgcc	aggaggctcc	agccataggg	gcctagtgtg	gccatcgagg	gacttgactt	1200
gtgtgtgttt	ctgaagtgtt	cgaggggtacc	aggagagctg	gcgatgactg	aactgctgat	1260
ggacaaatgc	tctgtgctct	ctagttagcc	ctgaatttgc	ttcctctgac	aagttacctc	1320
acctaatttt	tgcttctcag	gaatgagaat	ctttggccac	tggagagccc	ttgctcagtt	1380
ttctctattc	ttattattca	ctgcactata	ttctaagcac	ttacatgtgg	agatactgta	1440
acctgagggc	agaaaagcca	ntgtgtcatt	gtttacttgt	cctgtcactg	gatctgggct	1500

```
aaagtcctcc accaccactc tggacctaa gacctgggggt aagtgtgggt tgtgcatccc 1560
caatccagat aataaaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616
```

<400> 114

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
20 25 30

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
50 55 60

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
130 135 140

Val	Thr	Val	Glu	Trp	Leu	Arg	Val	Arg	Asp	Asp	Gly	Ser	Asn	Arg	Thr
145					150					155					160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
180 185 190

Pro	Arg	Gln	Pro	Leu	Leu	Leu	Gln	Val	Ser	Val	Gln	Arg	Glu	His	Leu
		195					200					205			

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
355 360 365

<210> 115
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 115
aggactgccca taacttgcct g 21

<210> 116
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 116
ataggagttg aagcagcgct gc 22

<210> 117
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 117
tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118
 <211> 1857
 <212> DNA
 <213> Homo sapiens

<400> 118
 gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60
 aaggcgcaag tcgagaggaa actgtttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180
 aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaaag 240
 tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
 gaggaccggg tgaccttctt gccaaactggt atcaccttca agtccgtgac acgggaagac 360
 actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
 gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctccctctgcc 480
 accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540
 tacacctggg tcaaagatgg gatagtgat cctacgaatc ccaaagcac ccgtgccttc 600
 agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tcccctgtca 660
 gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
 tcaaattgctg tgcgcatgga agctgtggag cggaatgtgg gggtcacgtg ggcagccgtc 780
 cttgtaaccc tgattctcct gggaatcttg gtttttggca tctggtttgc ctatagccga 840
 ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
 agtgcccga gtgaaggaga attcaaacag acctcgatc tcctgggtgtg agcctgggtcg 960
 gctcaccgcc tatcatctgc atttgcctta cttaggtgct accggactct ggcccctgat 1020
 gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc ccctacttct 1080
 tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
 tttcctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200
 agggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260
 tggcgggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaaat 1320
 aggtatcttg agcttggttc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380
 tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttgggtgat gacactgggg 1440
 tccttccatc tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500
 ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
 agctcttggt gtggagagca tagtaaat ttagagaact tgaagccaaa aggatttaaa 1620
 accgctgtc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
 cagaggctga ggcaggcggg tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
 ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtcatgc ctgtagtccc 1800
 agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

<210> 119
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 119
 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1 5 10 15
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 35 40 45
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 55 60

Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	
65					70					75					80	
Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu	Pro	Thr	Gly	Ile	Thr	Phe	
				85					90					95		
Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr	Gly	Thr	Tyr	Thr	Cys	Met	Val	Ser	
			100					105					110			
Glu	Glu	Gly	Gly	Asn	Ser	Tyr	Gly	Glu	Val	Lys	Val	Lys	Leu	Ile	Val	
		115					120					125				
Leu	Val	Pro	Pro	Ser	Lys	Pro	Thr	Val	Asn	Ile	Pro	Ser	Ser	Ala	Thr	
	130					135					140					
Ile	Gly	Asn	Arg	Ala	Val	Leu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	Ser	Pro	
145					150					155					160	
Pro	Ser	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	
				165					170					175		
Pro	Lys	Ser	Thr	Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Val	Leu	Asn	Pro	
			180					185					190			
Thr	Thr	Gly	Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	
		195					200					205				
Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Gly	Thr	Pro	Met	Thr	Ser	
	210					215					220					
Asn	Ala	Val	Arg	Met	Glu	Ala	Val	Glu	Arg	Asn	Val	Gly	Val	Ile	Val	
225					230					235					240	
Ala	Ala	Val	Leu	Val	Thr	Leu	Ile	Leu	Leu	Gly	Ile	Leu	Val	Phe	Gly	
				245					250					255		
Ile	Trp	Phe	Ala	Tyr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys	Lys	Gly	
			260					265					270			
Thr	Ser	Ser	Lys	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Ala	Arg	Ser	Glu	
		275					280					285				
Gly	Glu	Phe	Lys	Gln	Thr	Ser	Ser	Phe	Leu	Val						
	290					295										

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 120

tgcgagct gtgttctgtt tccc

<210> 121
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 121
 tgatcgcat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

 <210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 122
 acacctgggtt caaagatggg 20

 <210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 123
 taggaagagt tgctgaaggc acgg 24

 <210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 124
 ttgccttact caggtgctac 20

 <210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 125
actcagcagt ggtaggaaaag

20

<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens

<400> 126
cagcgcgtgg cccggcgccgc tgtgggggaca gcatgagcgg cggttggatg gcgcagggtg 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300
ggattgagcc atgtaccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgtgcga cggccacca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaagg gatgccaaa ccatggggcc ccctgtgacc ctggagagt 600
tcacctctct caggaatgcc acaaccatgg gggcccctgt gaccctggag agtgtcccct 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggc caccgccacc ctccctcttt 780
tgtcctggct ccgagcccag gagcgctcc gccactggg gttactggg gccatgaagg 840
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900
ccgtcactca gccctgggag tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020
tcctgcagaa gtggccctgg agattgaggg tccttggaac ctccctatgg agatccgggg 1080
agctaggatg gggaaacctgc cacagccaga actgaggggc tggcccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc 1210

<210> 127
<211> 282
<212> PRT
<213> Homo sapiens

<400> 127
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
1 5 10 15
Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
20 25 30
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
35 40 45
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
50 55 60
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
65 70 75 80
Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
85 90 95
Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
 225 230 235 240
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 129

ttggttcac agccgagctc gtcg

24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)..(1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cgggtctcgtc cgctcgcgca gcgggcggcag cagaggtcgc gcacagatgc 60
gggttagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagaccca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccgca 180
gcaatggaga tggatttcta gacgagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcgccct gcacagctca 300
cgggcgggtt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactc 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgtc 600
atgaaggatt caagatccg taccgagc tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctcctccc ggtggggact gtgatctcct 780
atcgctgctt tcccgattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggt gagtacgga gatttcgtct gccaccgag gccttgtgag cgctacaacc 960
acggaactgt ggtggagttt tactgcgac ctggctacag cctcaccag gactacaagt 1020
acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatacag 1080
agcaaactg gccagcacc catgagacc tctgaccac gtggaagatt gtggcggttca 1140
cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260
ttgtggtggt agacggcgtg cccgtcatgc tcccgctcta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttaggcccc gggtagatg cctctgtggg ccagggtgc cccttaccg 1380
tggacgacca gagccccca gcatacccg gctcagggga cacggacaca ggccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gtcctaaagt ctgtattcac 1500
ctcccagggt ccaagagagc accaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcattcatca tgcccactgg gtgttgttcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt ctttctcttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtagggg tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490
<212> PRT
<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln	
1				5					10					15		
Gln	Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val	
			20					25					30			
Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr	
		35					40					45				
Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu	
	50					55					60					
Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val	
65					70					75					80	
Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys	
				85					90						95	
Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser	
			100					105					110			
Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu	
		115					120					125				
Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile	
	130					135					140					
Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn	
145					150					155					160	
Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile	
				165					170					175		
Cys	Gln	Gly	Cys	Leu	Arg	Pro	Leu	Ala	Ser	Ser	Asn	Gly	Tyr	Val	Asn	
			180					185					190			
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr	
		195					200					205				
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys	
	210					215					220					
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu	
225					230					235					240	
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe	
				245					250					255		
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val	
			260					265					270			
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr	

275					280					285					
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys
290					295					300					
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr
305					310					315					
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu
325					330					335					
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His
340					345					350					
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe
355					360					365					
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala
370					375					380					
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val
385					390					395					
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr
405					410					415					
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys
420					425					430					
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro
435					440					445					
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile
450					455					460					
Ile	Ala	Ser	Thr	Ala	Glu	Glu	Val	Ala	Ser	Thr	Ser	Pro	Gly	Ile	His
465					470					475					
His	Ala	His	Trp	Val	Leu	Phe	Leu	Arg	Asn						
485					490										

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttacia aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggtcgcgtc gtggcctaga 60
gatgctgctg ccgcggttgc agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120
ccgtagcgcc cgagtgtcgg ggggcgccacc cgagtcgggc catgaggccg ggaaccgcgc 180
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc 240
tgagtgcctc ggatttggac ctacagaggag ggcagccagt ctgccgggga gggacacaga 300
ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagttag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcttgccgca 600
gcgaggtctg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccc 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctctctctcc 900
ttgtggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaagaag caacacacca tctggccctc tctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttctga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctccca gaccaaattg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380
ggaaaatata cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tccccacgac ctctgttgg accccacgt tttggctgta tcctttatcc cagccagtca 1500
tccagctcga ccttatgaga aggtacctg cccaggtctg gcacatagta gactctcaat 1560
aaatgtcact tggttggtt tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

<211> 382

<212> PRT

<213> Homo sapiens

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
1 5 10 15

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
35 40 45

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
65 70 75 80

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
100 105 110

Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
130 135 140

Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
165 170 175

Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
195 200 205

Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
225 230 235 240

Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
260 265 270

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 141
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgcgg acttgggggc gcccgcgtgag ccccggcgcc cgcagaagac 120
 ttgtgtttgc ctccctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360
 tcctctcaag ccgctccgcg tggaggagca ggtagagtgg aacccccagc tattagaggt 420
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600
 tgtggaagac attccctttc ttccaccaac cttcaaccga caggaggtct ttattcgttc 660
 cactaacatt tttcggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagt 720
 tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
 tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
 tagtgataaa gtggacttct tcctcctcct ggacaacgtg gctgccgagc aggcacacaa 960
 cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaaacaga gagctgtgga 1020
 cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggcc 1080
 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
 gaccctgggg atttttgacc acaaatggcc accgtttgct gttgacctga ccatggaact 1260
 ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
 ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
 agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
 gcctttatac aatg 1514

<210> 142
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 142
 Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
 1 5 10 15
 Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
 20 25 30
 Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
 35 40 45
 Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
 50 55 60
 Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
 65 70 75 80
 Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
 85 90 95

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu	
			100					105					110			
Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly	
		115					120					125				
Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val	
	130					135					140					
Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe	
145					150					155					160	
Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu	
				165					170					175		
Leu	Ala	Gly	Leu	Phe	Gln	Cys	Gln	Lys	Glu	Gly	Pro	Ile	Ile	Ile	His	
		180						185					190			
Thr	Asp	Glu	Ala	Asp	Ser	Glu	Val	Leu	Tyr	Pro	Asn	Tyr	Gln	Ser	Cys	
	195						200					205				
Trp	Ser	Leu	Arg	Gln	Arg	Thr	Arg	Gly	Arg	Arg	Gln	Thr	Ala	Ser	Leu	
	210					215					220					
Gln	Pro	Gly	Ile	Ser	Glu	Asp	Leu	Lys	Lys	Val	Lys	Asp	Arg	Met	Gly	
225					230					235					240	
Ile	Asp	Ser	Ser	Asp	Lys	Val	Asp	Phe	Phe	Ile	Leu	Leu	Asp	Asn	Val	
				245					250					255		
Ala	Ala	Glu	Gln	Ala	His	Asn	Leu	Pro	Ser	Cys	Pro	Met	Leu	Lys	Arg	
		260						265					270			
Phe	Ala	Arg	Met	Ile	Glu	Gln	Arg	Ala	Val	Asp	Thr	Ser	Leu	Tyr	Ile	
	275						280					285				
Leu	Pro	Lys	Glu	Asp	Arg	Glu	Ser	Leu	Gln	Met	Ala	Val	Gly	Pro	Phe	
	290					295					300					
Leu	His	Ile	Leu	Glu	Ser	Asn	Leu	Leu	Lys	Ala	Met	Asp	Ser	Ala	Thr	
305					310					315					320	
Ala	Pro	Asp	Lys	Ile	Arg	Lys	Leu	Tyr	Leu	Tyr	Ala	Ala	His	Asp	Val	
			325						330					335		
Thr	Phe	Ile	Pro	Leu	Leu	Met	Thr	Leu	Gly	Ile	Phe	Asp	His	Lys	Trp	
		340						345					350			
Pro	Pro	Phe	Ala	Val	Asp	Leu	Thr	Met	Glu	Leu	Tyr	Gln	His	Leu	Glu	
		355					360					365				
Ser	Lys	Glu	Trp	Phe	Val	Gln	Leu	Tyr	Tyr	His	Gly	Lys	Glu	Gln	Val	
	370					375					380					
Pro	Arg	Gly	Cys	Pro	Asp	Gly	Leu	Cys	Pro	Leu	Asp	Met	Phe	Leu	Asn	
385					390					395					400	

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

r

<400> 147

```
ctcctctttaa cataacttgca gctaaaaacta aatattgctg cttgggggacc tccttctagc 60
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaacccta gtggtatfff gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480
gagctctttc tccccagtc cagagggtgt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccgggcc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaacc ttcaggattg cccttctggg ccttggggga agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc ttgacttga gactagtagg 840
aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900
ctgtgatgac aactggggag aaaaggagga ccagggtggtg tgcaagcaac tgggctgtgg 960
gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccctgggg ttggccgcat 1020
ctggctggat aatgttcgtt gctcagggga ggagcagtcc ctggagcagt gccagcacag 1080
atthtggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgtg 1140
ggtgggcac atctaactctg ttgagtgcct gaatagaaga aaaacacaga agaaggggagc 1200
atthtactgt tacatgactg catgggatga aactgatct tcttctgccc ttggactggg 1260
acttatactt ggtgcccctg attctcaggc cttcagagtt ggatcagaac ttacaacatc 1320
aggtctagtt ctcaggccat cagacatagt ttggaactac atcaccacct ttcctatgtc 1380
tccacattgc acacagcaga ttcccagcct ccataattgt gtgtatcaac tacttaaata 1440
cattctcaca cacacacaca cacacacaca cacacacaca cacataca ccatttgtcc 1500
tgthtctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686
```

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

```
Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
  1             5             10             15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
  20             25             30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
  35             40             45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
  50             55             60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
  65             70             75             80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
  85             90             95
```


<400> 149
ttcagctcat caccttcacc tgcc 24

<210> 150
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 150
ggctcataca aaataccact aggg 24

<210> 151
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 151
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152
<211> 1427
<212> DNA
<213> Homo sapiens

<400> 152
actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60
accacgcgt ccgcggacgc gtgggcggac gcgtgggccc gctaccagga agagtctgcc 120
gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
cctgggcgtc ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240
gaatgctgtg gtggtgatca caggcgccac ctcagggtg ggcaaagaat gtgcaaaagt 300
cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420
ggtgaccttc gacctcacag actctggggc catagtgtga gcagcagctg agatcctgca 480
gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780
ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaagt ccatcaccgc 840
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900
ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
cttactgctt tccttggtctg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080
agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taataaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380

cttggccgcc atggcccaac ttgtttattg cagcttataa tggttac

1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr
210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val

260	265	270	
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu			
275	280	285	
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu			
290	295	300	
Arg Lys Ser Lys Asn Ser			
305	310		

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 154
 ggtgctaaac tggtgctctg tggc 24

<210> 155
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 155
 cagggaaga tgagcattcc 20

<210> 156
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 156
 tcatactgtt ccatctcggc acgc 24

<210> 157
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 157

aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc

50

<210> 158

<211> 1771

<212> DNA

<213> Homo sapiens

<400> 158

```
cccacgcgtc cgctggtggt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaa acacaccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120
cctcctgctt ctcccggttac tgategtctg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420
gaaggcagaa attggagatg ttagtatttt agtaaaatat gctggtgtag tctatacatc 480
agatttgttt gctacacaaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540
acatttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaactctg gcttcatcaa 780
aaatccaagt acaagtttgg gacccactct ggaacctgag gaagtggtaa acaggctgat 840
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080
cttctgtttt ttctaattat cccatttct tcaatatcat ttttgaggct ttggcagtct 1140
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260
taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320
ttattttaaca tatattttta tttttgattg cacttaaatt ttgtataatt tgtgtttctt 1380
tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440
tagtggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500
gccactctgt ttcttgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560
gctagagggt gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620
agagaatgta ccacaaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771
```

<210> 159

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

```
Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
  1                      5                      10                      15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
                20                      25                      30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
                35                      40                      45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
  50                      55                      60
```

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
 65 70 75 80
 Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
 85 90 95
 Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
 100 105 110
 Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
 115 120 125
 Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
 130 135 140
 Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
 145 150 155 160
 Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
 165 170 175
 Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
 180 185 190
 Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
 195 200 205
 Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
 210 215 220
 Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
 225 230 235 240
 Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
 245 250 255
 Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270
 Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285
 Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 161
atcccatgca tcagcctgtt tacc 24

<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 162
gctgggtgtag tctatacatc agatttgttt gctacacaag atcctcag 48

<210> 163
<211> 2076
<212> DNA
<213> Homo sapiens

<400> 163
cccacgcgtc cgcgagcgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 120
attgttttcg tggtcctgtt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct cacccttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttccagga 300
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttaca cagcaacctc 360
ttcttctggg tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420
caggttgggc cgggagggtt atccatgttt ggactctttg tggaacatgg gccttatgtt 480
gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660
atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
tatgcagaat tcctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900
aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggtttga ggcctttgaa 960
atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020
acaggatgta gtaattacta taactttttg cggtgcacgg aacctgagga tcagctttac 1080
tatgtgaaat ttttgtcact ccagagggtg agacaagcca tccacgtggg gaatcagact 1140
tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaa 1200
ccatggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260
atcatcgtgg cagctgcctt gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320
caggaataca agaaggcaga aaaaaagtt tggaagatct ttaaactctga cagtgaagtg 1380
gctggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440
attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500
aaaggatggg atccttatgt tgataaaact accttcccaa aagagaacat cagaggtttt 1560
cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620

```

tcatatctgc aagatTTTTT tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680
ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740
ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800
ttttaggggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860
taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920
gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

```

```

<210> 164
<211> 476
<212> PRT
<213> Homo sapiens

```

```

<400> 164
Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
  1             5             10             15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
      20             25             30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
      35             40             45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
      50             55             60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val
      65             70             75             80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
      85             90             95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro
      100            105            110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
      115            120            125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
      130            135            140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
      145            150            155            160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
      165            170            175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
      180            185            190

Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
      195            200            205

Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
      210            215            220

```


Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser	225	230	235	240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile	245	250	255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His	260	265	270	
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu	275	280	285	
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr	290	295	300	
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys	305	310	315	320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro	325	330	335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly	340	345	350	
Thr	Ile	Val	Glu	Lys	Tyr	Leu	Arg	Glu	Asp	Thr	Val	Gln	Ser	Val	Lys	355	360	365	
Pro	Trp	Leu	Thr	Glu	Ile	Met	Asn	Asn	Tyr	Lys	Val	Leu	Ile	Tyr	Asn	370	375	380	
Gly	Gln	Leu	Asp	Ile	Ile	Val	Ala	Ala	Ala	Leu	Thr	Glu	Arg	Ser	Leu	385	390	395	400
Met	Gly	Met	Asp	Trp	Lys	Gly	Ser	Gln	Glu	Tyr	Lys	Lys	Ala	Glu	Lys	405	410	415	
Lys	Val	Trp	Lys	Ile	Phe	Lys	Ser	Asp	Ser	Glu	Val	Ala	Gly	Tyr	Ile	420	425	430	
Arg	Gln	Ala	Gly	Asp	Phe	His	Gln	Val	Ile	Ile	Arg	Gly	Gly	Gly	His	435	440	445	
Ile	Leu	Pro	Tyr	Asp	Gln	Pro	Leu	Arg	Ala	Phe	Asp	Met	Ile	Asn	Arg	450	455	460	
Phe	Ile	Tyr	Gly	Lys	Gly	Trp	Asp	Pro	Tyr	Val	Gly	465	470	475					

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 165
ttccatgccca cctaagggag actc 24

<210> 166
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 166
tggatgaggt gtgcaatggc tggc 24

<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167
agctctcaga ggctggtcat aggg 24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
cgagggcttt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
atTTTTccct ttcctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120
tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180
tccttgccctc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtgaggt 240
gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300
cctggagagc ctggggggagg gcctgcctaa caagctttca aaaaacagga gcgacttcca 360
ctgggctggg ataagacgtg ccggtaggat agggaagact gggtttagtc ctaatatcaa 420
attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480
cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540
tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600
gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccctggg tcaggccagc ctctttgctc ctcccggaaa ttatttttgg 720

```

tctgaccact ctgccttgtg ttttgcagaa tcatgtgagg gccaacccggg gaaggtggag 780
cagatgagca cacacaggag ccgtctcctc accgccgccc ctctcagcat ggaacagagg 840
cagccctggc cccggggcct ggaggtggac agccgctctg tggtcctgct ctcagtggtc 900
tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960
aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020
ggggccatca accgggtcta taagctgaca ggcaacctga ccatccaggt ggctcataag 1080
acagggccag aagaggacaa caagtctcgt taccgcgcc tcatcgtgca gccctgcagc 1140
gaagtgtcga ccctcaccaa caatgtcaac aagctgctca tcattgacta ctctgagaac 1200
cgctgtctgg cctgtgggag cctctaccag ggggtctgca agctgctgcg gctggatgac 1260
ctcttcatcc tgggtggagcc atcccacaag aaggagcact acctgtccag tgtcaacaag 1320
acgggcacca tgtacggggg gattgtgcgc tctgaggggt aggatggcaa gctcttcatc 1380
ggcacggctg tggatgggaa gcaggattac ttcccgaccc tgtccagccg gaagctgcc 1440
cgagaccctg agtctcagc catgctcgac tatgagctac acagcgattt tgtctcctct 1500
ctcatcaaga tcccttcaga caccctggcc ctgggtctccc actttgacat cttctacatc 1560
tacggctttg ctagtggggg ctttgtctac ttctcactg tccagcccga gaccctgag 1620
ggtgtggcca tcaactccgc tggagacctc ttctacacct cacgcatcgt gcggctctgc 1680
aagtaggacc ccaagtcca ctcatacgtg tccctgccct tcggctgcac ccggggccggg 1740
gtggaatacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860
cagtatcacc acccgcccga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920
ttgcagatca aggagcgctt gcagtcctgc taccagggcg agggcaacct ggagctcaac 1980
tggctgctgg ggaaggacgt ccagtgcacg aaggcgctg tccccatcga tgataacttc 2040
tgtggactgg acatcaacca gcccctggga ggctcaactc cagtggaggg cctgaccctg 2100
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggctacagc 2160
gtggtttttg tggggactaa gagtggcaag ctgaaaaagg taagagtcta tgagttcaga 2220
tgctccaatg ccattcacct cctcagcaaa gagtccctct tggaaggtag ctattggtgg 2280
agatttaact ataggcaact ttattttctt ggggaacaaa ggtgaaatgg ggaggtaga 2340
aggggttaat tttgtgactt agcttctagc tacttcctcc agccatcagt cattgggtat 2400
gtaaggaatg caagcgtatt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460
acatctgcaa aagcaaa 2477

```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
 1             5             10             15

```

```

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20             25             30

```

```

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35             40             45

```

```

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50             55             60

```

```

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65             70             75             80

```

```

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85             90             95

```

```

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100            105            110

```

Thr	Gly	Ala	Val	Tyr	Val	Gly	Ala	Ile	Asn	Arg	Val	Tyr	Lys	Leu	Thr	115	120	125
Gly	Asn	Leu	Thr	Ile	Gln	Val	Ala	His	Lys	Thr	Gly	Pro	Glu	Glu	Asp	130	135	140
Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val	145	150	155
Leu	Thr	Leu	Thr	Asn	Asn	Val	Asn	Lys	Leu	Leu	Ile	Ile	Asp	Tyr	Ser	165	170	175
Glu	Asn	Arg	Leu	Leu	Ala	Cys	Gly	Ser	Leu	Tyr	Gln	Gly	Val	Cys	Lys	180	185	190
Leu	Leu	Arg	Leu	Asp	Asp	Leu	Phe	Ile	Leu	Val	Glu	Pro	Ser	His	Lys	195	200	205
Lys	Glu	His	Tyr	Leu	Ser	Ser	Val	Asn	Lys	Thr	Gly	Thr	Met	Tyr	Gly	210	215	220
Val	Ile	Val	Arg	Ser	Glu	Gly	Glu	Asp	Gly	Lys	Leu	Phe	Ile	Gly	Thr	225	230	235
Ala	Val	Asp	Gly	Lys	Gln	Asp	Tyr	Phe	Pro	Thr	Leu	Ser	Ser	Arg	Lys	245	250	255
Leu	Pro	Arg	Asp	Pro	Glu	Ser	Ser	Ala	Met	Leu	Asp	Tyr	Glu	Leu	His	260	265	270
Ser	Asp	Phe	Val	Ser	Ser	Leu	Ile	Lys	Ile	Pro	Ser	Asp	Thr	Leu	Ala	275	280	285
Leu	Val	Ser	His	Phe	Asp	Ile	Phe	Tyr	Ile	Tyr	Gly	Phe	Ala	Ser	Gly	290	295	300
Gly	Phe	Val	Tyr	Phe	Leu	Thr	Val	Gln	Pro	Glu	Thr	Pro	Glu	Gly	Val	305	310	315
Ala	Ile	Asn	Ser	Ala	Gly	Asp	Leu	Phe	Tyr	Thr	Ser	Arg	Ile	Val	Arg	325	330	335
Leu	Cys	Lys	Asp	Asp	Pro	Lys	Phe	His	Ser	Tyr	Val	Ser	Leu	Pro	Phe	340	345	350
Gly	Cys	Thr	Arg	Ala	Gly	Val	Glu	Tyr	Arg	Leu	Leu	Gln	Ala	Ala	Tyr	355	360	365
Leu	Ala	Lys	Pro	Gly	Asp	Ser	Leu	Ala	Gln	Ala	Phe	Asn	Ile	Thr	Ser	370	375	380
Gln	Asp	Asp	Val	Leu	Phe	Ala	Ile	Phe	Ser	Lys	Gly	Gln	Lys	Gln	Tyr	385	390	395
His	His	Pro	Pro	Asp	Asp	Ser	Ala	Leu	Cys	Ala	Phe	Pro	Ile	Arg	Ala	405	410	415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn
 450 455 460
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
 465 470 475 480
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
 485 490 495
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
 500 505 510
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
 515 520 525
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
 530 535 540
 Leu Tyr Phe Leu Gly Glu Gln Arg
 545 550

<210> 171
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 171
 tggaataccg cctcctgcag

20

<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 172
 cttctgccct ttggagaaga tggc

24

<210> 173
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173

ggactcactg gccaggcct tcaatatcac cagccaggac gat

43

<210> 174

<211> 3106

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1683)..(1683)

<223> a, t, c or g

<400> 174

aggctccccg	gcgcggtga	gtgcggactg	gagtgggaac	ccgggtcccc	gcgcttagag	60
aacacgcgat	gaccacgtgg	agcctccggc	ggaggccggc	ccgcacgctg	ggactcctgc	120
tgctggctgt	cttgggcttc	ctgggtgctc	gcaggctgga	ctggagcacc	ctgggtccctc	180
tgcggtctcc	ccatcgacag	ctggggctgc	aggccaaggg	ctggaacttc	atgctggagg	240
attccacctt	ctggatcttc	gggggtctca	tccactattt	ccgtgtgccc	agggagtact	300
ggagggaccg	cctgctgaag	atgaaggcct	gtggcttgaa	caccctcacc	acctatgttc	360
cgtggaacct	gcatgagcca	gaaagaggca	aatttgactt	ctctgggaac	ctggacctgg	420
aggccttcgt	cctgatggcc	gcagagatcg	ggctgtgggt	gattctgctg	ccaggcccct	480
acatctgcag	tgagatggac	ctcgggggct	tgcccagctg	gctactccaa	gaccctggca	540
tgaggctgag	gacaacttac	aagggtctca	ccgaagcagt	ggacctttat	tttgaccacc	600
tgatgtccag	ggtggtgcca	ctccagtaca	agcgtggggg	acctatcatt	gccgtgcagg	660
tggagaatga	atatggttcc	tataataaag	accccgcata	catgccctac	gtcaagaagg	720
cactggagga	ccgtggcatt	gtggaactgc	tcctgacttc	agacaacaag	gatgggctga	780
gcaaggggat	tgtccagggg	gtcttgccca	ccatcaactt	gcagtcaaca	cacgagctgc	840
agctactgac	cacctttctc	ttcaacgtcc	aggggactca	gccaagatg	gtgatggagt	900
actggacggg	gtggtttgac	tcgtggggag	gcctcacaa	tatcttggat	tcttctgagg	960
ttttgaaaac	cgtgtctgcc	attgtggacg	ccggctcctc	catcaacctc	tacatgttcc	1020
acggaggcac	caactttggc	ttcatgaatg	gagccatgca	cttccatgac	tacaagtacg	1080
atgtcaccag	ctatgactat	gatgctgtgc	tgacagaagc	cggcgattac	acggccaagt	1140
acatgaagct	tcgagacttc	ttcggctcca	tctcaggcat	ccctctccct	ccccacctg	1200
accttcttcc	caagatgccg	tatgagccct	taacgccagt	cttgtacctg	tctctgtggg	1260
acgccctcaa	gtacctgggg	gagccaatca	agtctgaaaa	gcccataaac	atggagaacc	1320
tgccagtcaa	tgggggaaat	ggacagtcct	tcgggtacat	tctctatgag	accagcatca	1380
cctcgtctgg	catcctcagt	ggccacgtgc	atgatcgggg	gcagggtgtt	gtgaacacag	1440
tatccatagg	attcttggac	tacaagacaa	cgaagattgc	tgtccccctg	atccaggggt	1500
acaccgtgct	gaggatcttg	gtggagaatc	gtgggcgagt	caactatggg	gagaatattg	1560
atgaccagcg	caaaggctta	attggaaatc	tctatctgaa	tgattcacc	ctgaaaaact	1620
tcagaatcta	tagcctggat	atgaagaaga	gcttctttca	gagggttcgg	ctggacaaat	1680
gngtccct	cccagaaaca	cccacattac	ctgctttctt	cttgggtagc	ttgtccatca	1740
gctccacgcc	ttgtgacacc	tttctgaagc	tggagggctg	ggagaagggg	gttgtattca	1800
tcaatggcca	gaaccttggg	cgttactgga	acattggacc	ccagaagacg	ctttacctcc	1860
caggtccctg	gttgagcagc	ggaatcaacc	aggtcatcgt	ttttgaggag	acgatggcgg	1920
gccctgcatt	acagttcacg	gaaaccccc	acctgggcag	gaaccagtac	attaagttag	1980
cgggtggcacc	cctcctgct	ggtgccagt	ggagactgcc	gcctcctctt	gacctgaagc	2040
ctggtggctg	ctgccccacc	cctcactgca	aaagcatctc	cttaagtagc	aacctcaggg	2100
actgggggct	acagctctgc	cctgtctcag	ctcaaaacct	taagcctgca	gggaaagggt	2160
ggatggctct	gggctggct	ttgttgatga	tggttttctt	acagccctgc	tcttgtgccg	2220
aggctgtcgg	gctgtctcta	gggtgggagc	agctaatac	atcgcccagc	ctttggccct	2280

```

cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcattctgctg 2340
gactcaggcg tgctctttgc tggttcctgg gaggtctggc cacatccctc atggcccat 2400
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520
ctcggcgtga gaaacatgtg acttccccctt tcccttccca ctcgctgctt cccacagggt 2580
gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcagggtg 2640
ctctgggtgtt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga agccatggcc 2760
catgtctgca catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccaggga ggaggacaga aggcccagct cacatgtgag 2880
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggcccagct 2940
cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000
gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060
ggctcactgt cctgagttgc agtaaagcta taaccttgaa tcacaa 3106

```

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1           5           10           15

```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
          20           25           30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
      35           40           45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
      50           55           60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
      65           70           75           80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
          85           90           95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
      100           105           110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
      115           120           125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
      130           135           140

```

```

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
      145           150           155           160

```

```

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp

```

165								170				175			
His	Leu	Met	Ser	Arg	Val	Val	Pro	Leu	Gln	Tyr	Lys	Arg	Gly	Gly	Pro
			180					185					190		
Ile	Ile	Ala	Val	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Asn	Lys	Asp
		195					200					205			
Pro	Ala	Tyr	Met	Pro	Tyr	Val	Lys	Lys	Ala	Leu	Glu	Asp	Arg	Gly	Ile
	210					215					220				
Val	Glu	Leu	Leu	Leu	Thr	Ser	Asp	Asn	Lys	Asp	Gly	Leu	Ser	Lys	Gly
225					230					235					240
Ile	Val	Gln	Gly	Val	Leu	Ala	Thr	Ile	Asn	Leu	Gln	Ser	Thr	His	Glu
				245					250					255	
Leu	Gln	Leu	Leu	Thr	Thr	Phe	Leu	Phe	Asn	Val	Gln	Gly	Thr	Gln	Pro
			260					265					270		
Lys	Met	Val	Met	Glu	Tyr	Trp	Thr	Gly	Trp	Phe	Asp	Ser	Trp	Gly	Gly
	275						280					285			
Pro	His	Asn	Ile	Leu	Asp	Ser	Ser	Glu	Val	Leu	Lys	Thr	Val	Ser	Ala
	290					295					300				
Ile	Val	Asp	Ala	Gly	Ser	Ser	Ile	Asn	Leu	Tyr	Met	Phe	His	Gly	Gly
305					310					315					320
Thr	Asn	Phe	Gly	Phe	Met	Asn	Gly	Ala	Met	His	Phe	His	Asp	Tyr	Lys
				325					330					335	
Ser	Asp	Val	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Val	Leu	Thr	Glu	Ala	Gly
			340						345				350		
Asp	Tyr	Thr	Ala	Lys	Tyr	Met	Lys	Leu	Arg	Asp	Phe	Phe	Gly	Ser	Ile
		355					360					365			
Ser	Gly	Ile	Pro	Leu	Pro	Pro	Pro	Pro	Asp	Leu	Leu	Pro	Lys	Met	Pro
	370					375					380				
Tyr	Glu	Pro	Leu	Thr	Pro	Val	Leu	Tyr	Leu	Ser	Leu	Trp	Asp	Ala	Leu
385					390					395					400
Lys	Tyr	Leu	Gly	Glu	Pro	Ile	Lys	Ser	Glu	Lys	Pro	Ile	Asn	Met	Glu
				405					410					415	
Asn	Leu	Pro	Val	Asn	Gly	Gly	Asn	Gly	Gln	Ser	Phe	Gly	Tyr	Ile	Leu
			420				425						430		
Tyr	Glu	Thr	Ser	Ile	Thr	Ser	Ser	Gly	Ile	Leu	Ser	Gly	His	Val	His
		435					440					445			
Asp	Arg	Gly	Gln	Val	Phe	Val	Asn	Thr	Val	Ser	Ile	Gly	Phe	Leu	Asp
	450					455					460				
Tyr	Lys	Thr	Thr	Lys	Ile	Ala	Val	Pro	Leu	Ile	Gln	Gly	Tyr	Thr	Val

465		470		475		480
Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn						
		485		490		495
Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp						
		500		505		510
Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser						
		515		520		525
Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr						
		530		535		540
Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr						
		545		550		555
Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val						
		565		570		575
Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln						
		580		585		590
Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln						
		595		600		605
Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr						
		610		615		620
Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys						
		625		630		635

<210> 176
 <211> 2505
 <212> DNA
 <213> Homo sapiens

<400> 176

ggggacgcgg	agctgagagg	ctccgggcta	gctaggtgta	gggggtggacg	gggtcccagga	60
ccctggtgag	ggttctctac	ttggccttcg	gtgggggtca	agacgcaggc	acctacgccca	120
aaggggagca	aagccgggct	cggcccgagg	ccccaggac	ctccatctcc	caatgttgga	180
ggaatccgac	acgtgacggg	ctgtccgccc	tctcagacta	gaggagcgc	gtaaacgccca	240
tggtctccaa	gaagctgtcc	tgccttcggt	ccctgctgct	gccgctcagc	ctgacgctac	300
tgctgcccc	ggcagacact	cggtcggttcg	tagtggatag	gggtcatgac	cggtttctcc	360
tagacggggc	cccgttcg	tatgtgtctg	gcagcctgca	ctactttcgg	gtaccgcggg	420
tgctttgggc	cgaccgggct	ttgaagatgc	gatggagcgg	cctcaacgcc	atacagtttt	480
atgtgccctg	gaactaccac	gagccacagc	ctgggggtcta	taactttaat	ggcagccggg	540
acctcattgc	ctttctgaat	gaggcagctc	tagcgaacct	gttggtcata	ctgagaccag	600
gaccttacat	ctgtgcagag	tgggagatgg	gggggtctccc	atcctgggtg	cttcgaaaac	660
ctgaaattca	tctaagaacc	tcagatccag	acttccttgc	cgcagtggac	tcctggttca	720
aggtcttgct	gcccagata	tatccatggc	tttatcacia	tgggggcaac	atcattagca	780
ttcaggtgga	gaatgaatat	ggtagctaca	gagcctgtga	cttcagctac	atgaggcact	840
tggtctgggc	cttcctgtca	ctgctaggag	aaaagatctt	gctcttcacc	acagatgggc	900
ctgaaggact	caagtgtggc	tccttcggg	gactctatac	cactgtagat	tttggcccag	960
ctgacaacat	gacaaaaatc	tttaccctgc	ttcgggaagta	tgaaccccat	gggccattgg	1020
taaactctga	gtactacaca	ggctggctgg	attactgggg	ccagaatcac	tccacacggg	1080
ctgtgtcagc	tgtaaccaa	ggactagaga	acatgctcaa	gttgggagcc	agtgtgaaca	1140

```

tgtacatggt ccatggaggt accaactttg gatattggaa tgggtgccgat aagaagggac 1200
gcttccttcc gattactacc agctatgact atgatgcacc tataatctgaa gcaggggacc 1260
ccacacctaa gcttttttgc cttcgagatg tcatcagcaa gttccaggaa gttccttttg 1320
gacctttacc tcccccgagc cccaagatga tgcttggacc tgtgactctg cacctggttg 1380
ggcattttact ggcttttcta gacttgcttt gcccccgagg gccattcat tcaatcttgc 1440
caatgacctt tgaggctgtc aagcaggacc atgggttcat gttgtaccga acctatatga 1500
cccataccat ttttgagcca acaccattct gggtgccaaa taatggagtc catgaccgtg 1560
cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatatg agagacaaac 1620
tatttttgac ggggaaactg ggttccaaac tggatatctt ggtggagaac atggggaggc 1680
tcagcttttg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740
aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800
ggtttccctt ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattct 1860
actccaaaac atttccaatt ttaggtcag ttggggacac atttctatat ctacctggat 1920
ggaccaaggg ccaagctctg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980
ggccacaaca gacctctac gtgccaagat tcctgctgtt tcctagggga gccctcaaca 2040
aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100
agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
atacactgag tgcctctgaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220
ggtggctcat gcctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340
aaattagccg ggcgtgatgg tgggcacctc taatcccagc tacttgggag gctgagggca 2400
ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggaggttgt accactgcac 2460
tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

```

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

```

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1              5              10              15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
      20              25              30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
  35              40              45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
  50              55              60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
  65              70              75              80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
      85              90              95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
      100              105              110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
      115              120              125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
      130              135              140

```

Leu	Arg	Thr	Ser	Asp	Pro	Asp	Phe	Leu	Ala	Ala	Val	Asp	Ser	Trp	Phe	145	150	155	160
Lys	Val	Leu	Leu	Pro	Lys	Ile	Tyr	Pro	Trp	Leu	Tyr	His	Asn	Gly	Gly	165	170	175	
Asn	Ile	Ile	Ser	Ile	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Arg	Ala	180	185	190	
Cys	Asp	Phe	Ser	Tyr	Met	Arg	His	Leu	Ala	Gly	Leu	Phe	Arg	Ala	Leu	195	200	205	
Leu	Gly	Glu	Lys	Ile	Leu	Leu	Phe	Thr	Thr	Asp	Gly	Pro	Glu	Gly	Leu	210	215	220	
Lys	Cys	Gly	Ser	Leu	Arg	Gly	Leu	Tyr	Thr	Thr	Val	Asp	Phe	Gly	Pro	225	230	235	240
Ala	Asp	Asn	Met	Thr	Lys	Ile	Phe	Thr	Leu	Leu	Arg	Lys	Tyr	Glu	Pro	245	250	255	
His	Gly	Pro	Leu	Val	Asn	Ser	Glu	Tyr	Tyr	Thr	Gly	Trp	Leu	Asp	Tyr	260	265	270	
Trp	Gly	Gln	Asn	His	Ser	Thr	Arg	Ser	Val	Ser	Ala	Val	Thr	Lys	Gly	275	280	285	
Leu	Glu	Asn	Met	Leu	Lys	Leu	Gly	Ala	Ser	Val	Asn	Met	Tyr	Met	Phe	290	295	300	
His	Gly	Gly	Thr	Asn	Phe	Gly	Tyr	Trp	Asn	Gly	Ala	Asp	Lys	Lys	Gly	305	310	315	320
Arg	Phe	Leu	Pro	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Ser	325	330	335	
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile	340	345	350	
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro	355	360	365	
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu	370	375	380	
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu	385	390	395	400
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr	405	410	415	
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val	420	425	430	
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val	435	440	445	

Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr
 450 455 460
 Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg
 465 470 475 480
 Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro
 485 490 495
 Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu
 500 505 510
 Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys
 515 520 525
 Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr
 530 535 540
 Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly
 545 550 555 560
 Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr
 565 570 575
 Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu
 580 585 590
 Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu
 595 600 605
 Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu
 610 615 620
 Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640
 Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 178

tggtactcc aagacctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

<210> 182

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 182

tggcacccag aatggtggtg gctc

24

<210> 183

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 183

cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 184

```
gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60
gcaccacaaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120
gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180
aatattcttt cgaaaaagtc agagaagaga gcagttttag tgacattcca gatgtcaaaa 240
acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcggt 300
ttgggtgtgt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360
agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420
tgcatctgtt catgctgtcg ggggtgcccc atgctgtctt tgacctcaca gacctggatg 480
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
acctccaaga gctccacctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600
ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660
cctgggtgta tttgtcaaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840
caaagttagt cattcataat gacggcacta aactcctggg actgaacagc cttagaagaaa 900
tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020
aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080
aaattgttac tattcctccc tctattaccg atgtcaaaaa cttggagtca ctttatttct 1140
ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcagatgct 1200
tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260
tgcagcattt gcatactact gggaacaaag tggacattct gccaaaacaa ttgtttaaat 1320
gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
cagcccagct gggccagtggt cggatgctca agaaaagcgg gcttggttggt gaagatcacc 1500
tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560
ttgcaaatgg gatttaaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620
agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680
cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
aatgtttgta gggttttaag tcattcattt ccaaattcatt tttttttttc ttttggggaa 1800
aggggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaattgct tgctgtctaa agtaaatgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaa 1947
```

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

```
Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1             5             10             15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
      20             25             30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
      35             40             45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
      50             55             60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
      65             70             75             80
```

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His	
				85					90					95		
Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln	
			100					105					110			
Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala	
		115					120					125				
Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	
	130					135					140					
Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu	
145					150					155					160	
Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser	
				165					170					175		
Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val	
			180					185					190			
Ala	Glu	Ile	Pro	Ala	Trp	Val	Tyr	Leu	Leu	Lys	Asn	Leu	Arg	Glu	Leu	
		195					200					205				
Tyr	Leu	Ile	Gly	Asn	Leu	Asn	Ser	Glu	Asn	Asn	Lys	Met	Ile	Gly	Leu	
	210					215					220					
Glu	Ser	Leu	Arg	Glu	Leu	Arg	His	Leu	Lys	Ile	Leu	His	Val	Lys	Ser	
225					230					235					240	
Asn	Leu	Thr	Lys	Val	Pro	Ser	Asn	Ile	Thr	Asp	Val	Ala	Pro	His	Leu	
				245					250					255		
Thr	Lys	Leu	Val	Ile	His	Asn	Asp	Gly	Thr	Lys	Leu	Leu	Val	Leu	Asn	
			260					265					270			
Ser	Leu	Lys	Lys	Met	Met	Asn	Val	Ala	Glu	Leu	Glu	Leu	Gln	Asn	Cys	
		275					280					285				
Glu	Leu	Glu	Arg	Ile	Pro	His	Ala	Ile	Phe	Ser	Leu	Ser	Asn	Leu	Gln	
	290					295					300					
Glu	Leu	Asp	Leu	Lys	Ser	Asn	Asn	Ile	Arg	Thr	Ile	Glu	Glu	Ile	Ile	
305					310					315					320	
Ser	Phe	Gln	His	Leu	Lys	Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	His	Asn	
				325					330					335		
Lys	Ile	Val	Thr	Ile	Pro	Pro	Ser	Ile	Thr	His	Val	Lys	Asn	Leu	Glu	
			340					345					350			
Ser	Leu	Tyr	Phe	Ser	Asn	Asn	Lys	Leu	Glu	Ser	Leu	Pro	Val	Ala	Val	
		355					360					365				
Phe	Ser	Leu	Gln	Lys	Leu	Arg	Cys	Leu	Asp	Val	Ser	Tyr	Asn	Asn	Ile	
		370				375					380					

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr
465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
485 490 495

Phe Ala Asn Gly Ile
500

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 186

cctccctcta ttacccatgt c

21

<210> 187

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 187

gaccaacttt ctctgggagt gagg

24

<210> 188

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 188

gtcacttttat ttctctaaca acaagctcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

cccacgcgtc	cggccttctc	tctggacttt	gcattttccat	tccttttcat	tgacaaactg	60
acttttttta	tttctttttt	tccatctctg	ggccagcttg	ggatcctagg	ccgccctggg	120
aagacatttg	tgttttacac	acataaggat	ctgtgttttg	ggtttcttct	tcctcccctg	180
acattggcat	tgcttagtgg	ttgtgtgggg	agggagacca	cgtgggctca	gtgcttgctt	240
gcacttatct	gcctaggtac	atcgaagtct	tttgacctcc	atacagtgat	tatgcctgtc	300
atcgctgggtg	gtatcctggc	ggccttgctc	ctgctgatag	ttgtcgtgct	ctgtctttac	360
ttcaaaaatac	acaacgcgct	aaaagctgca	aaggaacctg	aagctgtggc	tgtaaaaaat	420
cacaaccag	acaagggtg	gtgggccaag	aacagccagg	ccaaaaccat	tgccacggag	480
tcttgtcctg	ccctgcagtg	ctgtgaagga	tatagaatgt	gtgccagttt	tgattccctg	540
ccaccttgct	gttgcgacat	aaatgagggc	ctctgagtta	ggaaaggctc	ccttctcaaa	600
gcagagccct	gaagacttca	atgatgtcaa	tgaggccacc	tgtttgtgat	gtgcaggcac	660
agaagaaagg	cacagctccc	catcagtttc	atggaaaata	actcagtgcc	tgctgggaac	720
cagctgctgg	agatccctac	agagagcttc	cactgggggc	aacccttcca	ggaaggagtt	780
ggggagagag	aaccctcact	gtggggaatg	ctgataaacc	agtcacacag	ctgctctatt	840
ctcacacaaa	tctaccctt	gcgtggctgg	aactgacgtt	tccttgagg	tgtccagaaa	900
gctgatgtaa	cacagagcct	ataaaagctg	tcggtcctta	aggctgcca	gcgccttgcc	960
aaaatggagc	ttgtaagaag	gctcatgcc	ttgaccctct	taattctctc	ctgtttggcg	1020
gagctgacaa	tggcggaggc	tgaaggcaat	gcaagctgca	cagtcagtct	agggggtgcc	1080
aatatggcag	agaccacaaa	agccatgatc	ctgcaactca	atcccagtga	gaactgcacc	1140
tggacaatag	aaagaccaga	aaacaaaagc	atcagaatta	tcttttcccta	tgtccagctt	1200
gatccagatg	gaagctgtga	aagtgaanaa	attaaagtct	ttgacggaac	ctccagcaat	1260
gggcctctgc	tagggcaagt	ctgcagtaaa	aacgactatg	ttcctgtatt	tgaatcatca	1320
tccagtacat	tgacgtttca	aatagttact	gactcagcaa	gaattcaaag	aactgtcttt	1380
gtcttctact	acttcttctc	tcctaacatc	tctattccaa	actgtggcgg	ttacctggat	1440
accttgaag	gaccttcac	cagccccaat	tacccaaagc	cgcatcctga	gctggcttat	1500
tgtgtgtggc	acatacaagt	ggagaaagat	tacaaagata	aactaaactt	caaagagact	1560
ttctagaaa	tagacaaaac	gtgcaaat	gattttcttg	ccatctatga	tggcccctcc	1620
accaactctg	gcctgattgg	acaagtctgt	ggcgtgtga	ctcccacctt	cgaatcgtca	1680
tcaaaactctc	tgactgtcgt	gttgtctaca	gattatgcca	attcttaccg	gggattttct	1740
gcttctctaca	cctcaattta	tgcagaaaac	atcaacacta	catctttaac	ttgtcttctt	1800
gacaggatga	gagttattat	aagcaaatcc	tacctagagg	cttttaactc	taatgggaat	1860
aacttgcaac	taaaagaccc	aacttgcaga	ccaaaattat	caaagtgtgt	ggaattttct	1920
gtccctctta	atggatgtgg	tacaatcaga	aaggtagaag	atcagtcaat	tacttacacc	1980
aatataatca	ccttttctgc	atcctcaact	tctgaagtga	tcacccgtca	gaaacaactc	2040
cagattattg	tgaagtgtga	aatgggacat	aattctacag	tggagataat	atacataaca	2100
gaagatgatg	taatacaaa	tcaaaatgca	ctgggcaaat	ataacaccag	catggctctt	2160
tttgaatcca	attcatattga	aaagactata	cttgaatcac	catattatgt	ggatttgaac	2220
caaactcttt	ttgttcaagt	tagtctgcac	acctcagatc	caaatttggg	ggtgtttctt	2280
gatacctgta	gagcctctcc	cacctctgac	tttgcattct	caacctacga	cctaatacaag	2340
agtggatgta	gtcgagatga	aacttgtga	gtgtatccct	tatttggaca	ctatgggaga	2400
ttccagttta	atgcctttaa	attcttgaga	agtatgagct	ctgtgtatct	gcagtgtaaa	2460
gttttgatat	gtgatagcag	tgaccaccag	tctcgtgca	atcaagggtg	tgtctccaga	2520
agcaaacgag	acatttcttc	atataaatgg	aaaacagatt	ccatcatagg	acccattcgt	2580
ctgaaaaggg	atcgaagtgc	aagtggcaat	tcaggatttc	agcatgaaac	acatgcgga	2640
gaaactccaa	accagccttt	caacagtgtg	catctgtttt	ccttcatggg	tctagctctg	2700
aatgtgggtga	ctgtagcgac	aatcacagtg	aggcattttg	taaatcaacg	ggcagactac	2760
aaataccaga	agctgcagaa	ctattaacta	acaggtccaa	ccctaagtga	gacatgtttc	2820

tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880
 ggctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

<210> 190
 <211> 607
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1 5 10 15
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
 20 25 30
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255

Gly	Phe	Ser	Ala	Ser	Tyr	Thr	Ser	Ile	Tyr	Ala	Glu	Asn	Ile	Asn	Thr	
			260					265					270			
Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys	
		275					280					285				
Ser	Tyr	Leu	Glu	Ala	Phe	Asn	Ser	Asn	Gly	Asn	Asn	Leu	Gln	Leu	Lys	
	290					295					300					
Asp	Pro	Thr	Cys	Arg	Pro	Lys	Leu	Ser	Asn	Val	Val	Glu	Phe	Ser	Val	
305					310					315					320	
Pro	Leu	Asn	Gly	Cys	Gly	Thr	Ile	Arg	Lys	Val	Glu	Asp	Gln	Ser	Ile	
				325					330					335		
Thr	Tyr	Thr	Asn	Ile	Ile	Thr	Phe	Ser	Ala	Ser	Ser	Thr	Ser	Glu	Val	
			340					345						350		
Ile	Thr	Arg	Gln	Lys	Gln	Leu	Gln	Ile	Ile	Val	Lys	Cys	Glu	Met	Gly	
		355					360					365				
His	Asn	Ser	Thr	Val	Glu	Ile	Ile	Tyr	Ile	Thr	Glu	Asp	Asp	Val	Ile	
	370					375					380					
Gln	Ser	Gln	Asn	Ala	Leu	Gly	Lys	Tyr	Asn	Thr	Ser	Met	Ala	Leu	Phe	
385					390					395					400	
Glu	Ser	Asn	Ser	Phe	Glu	Lys	Thr	Ile	Leu	Glu	Ser	Pro	Tyr	Tyr	Val	
				405					410					415		
Asp	Leu	Asn	Gln	Thr	Leu	Phe	Val	Gln	Val	Ser	Leu	His	Thr	Ser	Asp	
			420					425					430			
Pro	Asn	Leu	Val	Val	Phe	Leu	Asp	Thr	Cys	Arg	Ala	Ser	Pro	Thr	Ser	
		435					440					445				
Asp	Phe	Ala	Ser	Pro	Thr	Tyr	Asp	Leu	Ile	Lys	Ser	Gly	Cys	Ser	Arg	
	450					455					460					
Asp	Glu	Thr	Cys	Lys	Val	Tyr	Pro	Leu	Phe	Gly	His	Tyr	Gly	Arg	Phe	
465					470					475					480	
Gln	Phe	Asn	Ala	Phe	Lys	Phe	Leu	Arg	Ser	Met	Ser	Ser	Val	Tyr	Leu	
				485					490					495		
Gln	Cys	Lys	Val	Leu	Ile	Cys	Asp	Ser	Ser	Asp	His	Gln	Ser	Arg	Cys	
			500					505					510			
Asn	Gln	Gly	Cys	Val	Ser	Arg	Ser	Lys	Arg	Asp	Ile	Ser	Ser	Tyr	Lys	
		515					520					525				
Trp	Lys	Thr	Asp	Ser	Ile	Ile	Gly	Pro	Ile	Arg	Leu	Lys	Arg	Asp	Arg	
	530					535					540					
Ser	Ala	Ser	Gly	Asn	Ser	Gly	Phe	Gln	His	Glu	Thr	His	Ala	Glu	Glu	
545					550					555					560	

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val
565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr
595 600 605

<210> 191
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191
tctctattcc aaactgtggc g 21

<210> 192
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 192
tttgatgacg attcgaaggt gg 22

<210> 193
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194
<211> 2362
<212> DNA
<213> Homo sapiens

<400> 194
gacggaagaa cagcgctccc gagggccgcg gagcctgcag agaggacagc cggcctgcgc 60
cgggacatgc ggccccagga gctccccagg ctgcggttcc cggttgctgct gttgctgttg 120
ctgctgctgc cgccgcccgc gtgcccgcg cacagcgcca cgcgcttcga cccacactgg 180
gagtccttgg acgcccgcga gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240
atccactggg gagtggtttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360

```

aaatatgaag atttttgacc actattttaca gcaaaatttt ttaatgccaa ccagtgggca 420
gatatttttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccaag 540
agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttggg 600
ctgtactatt ccttttttga atggtttcat ccgctcttcc ttgaggatga atccagttca 660
ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720
aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780
aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtagtc 840
accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900
gatcgttata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960
aaactgtcct ggggctatag gaggaagct ggaatctctg actatcttac aattgaagaa 1020
ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttgat gaatattggg 1080
cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtgggggcc 1140
tggctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200
actgtcacc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260
tttcttaaat ggccacatc aggacagctg ttccttggcc atcccaaagc tattctgggg 1320
gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380
aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440
tgggctctag ccctaactaa tgtgatctaa agtgcagcag agtggctgat gctgcaagtt 1500
atgtctaagg ctaggaaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560
aactggataa gaaaattatt tggcagttca gccctttccc tttttccac taaatttttc 1620
ttaaattacc catgtaacca ttttaactct ccagtgcact ttgccattaa agtctcttca 1680
cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740
gaattggtgg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800
tatatagtta tgcatcactt aatatgggga tattttctgg gaaatgcatt gctagtcaat 1860
ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
cacaccta at gtgtatggta tagactgttg ctctaggct acagacatat acagcatgtt 1980
actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040
gagaaggtac agtaaaaata ctgtaaaaata aatggtgcac ctgtataggg cacttaccac 2100
gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgagtga tgtgaaggcc 2160
taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
caaacgtttt aattttttaa accttttttg ctcttttgta ataacactta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa 2362

```

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro

85					90					95					
Ser	Phe	Lys	Tyr	Glu	Asp	Phe	Gly	Pro	Leu	Phe	Thr	Ala	Lys	Phe	Phe
			100					105					110		
Asn	Ala	Asn	Gln	Trp	Ala	Asp	Ile	Phe	Gln	Ala	Ser	Gly	Ala	Lys	Tyr
		115					120					125			
Ile	Val	Leu	Thr	Ser	Lys	His	His	Glu	Gly	Phe	Thr	Leu	Trp	Gly	Ser
	130					135					140				
Glu	Tyr	Ser	Trp	Asn	Trp	Asn	Ala	Ile	Asp	Glu	Gly	Pro	Lys	Arg	Asp
145					150					155					160
Ile	Val	Lys	Glu	Leu	Glu	Val	Ala	Ile	Arg	Asn	Arg	Thr	Asp	Leu	Arg
				165					170					175	
Phe	Gly	Leu	Tyr	Tyr	Ser	Leu	Phe	Glu	Trp	Phe	His	Pro	Leu	Phe	Leu
		180						185					190		
Glu	Asp	Glu	Ser	Ser	Ser	Phe	His	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys
		195					200					205			
Thr	Leu	Pro	Glu	Leu	Tyr	Glu	Leu	Val	Asn	Asn	Tyr	Gln	Pro	Glu	Val
	210					215					220				
Leu	Trp	Ser	Asp	Gly	Asp	Gly	Gly	Ala	Pro	Asp	Gln	Tyr	Trp	Asn	Ser
225					230					235					240
Thr	Gly	Phe	Leu	Ala	Trp	Leu	Tyr	Asn	Glu	Ser	Pro	Val	Arg	Gly	Thr
			245						250					255	
Val	Val	Thr	Asn	Asp	Arg	Trp	Gly	Ala	Gly	Ser	Ile	Cys	Lys	His	Gly
			260					265					270		
Gly	Phe	Tyr	Thr	Cys	Ser	Asp	Arg	Tyr	Asn	Pro	Gly	His	Leu	Leu	Pro
		275					280					285			
His	Lys	Trp	Glu	Asn	Cys	Met	Thr	Ile	Asp	Lys	Leu	Ser	Trp	Gly	Tyr
		290				295					300				
Arg	Arg	Glu	Ala	Gly	Ile	Ser	Asp	Tyr	Leu	Thr	Ile	Glu	Glu	Leu	Val
305					310					315					320
Lys	Gln	Leu	Val	Glu	Thr	Val	Ser	Cys	Gly	Gly	Asn	Leu	Leu	Met	Asn
				325					330					335	
Ile	Gly	Pro	Thr	Leu	Asp	Gly	Thr	Ile	Ser	Val	Val	Phe	Glu	Glu	Arg
			340					345					350		
Leu	Arg	Gln	Val	Gly	Ser	Trp	Leu	Lys	Val	Asn	Gly	Glu	Ala	Ile	Tyr
		355					360					365			
Glu	Thr	Tyr	Thr	Trp	Arg	Ser	Gln	Asn	Asp	Thr	Val	Thr	Pro	Asp	Val
	370					375					380				
Trp	Tyr	Thr	Ser	Lys	Pro	Lys	Glu	Lys	Leu	Val	Tyr	Ala	Ile	Phe	Leu

385		390		395		400									
Lys	Trp	Pro	Thr	Ser	Gly	Gln	Leu	Phe	Leu	Gly	His	Pro	Lys	Ala	Ile
				405					410					415	
Leu	Gly	Ala	Thr	Glu	Val	Lys	Leu	Leu	Gly	His	Gly	Gln	Pro	Leu	Asn
			420					425					430		
Trp	Ile	Ser	Leu	Glu	Gln	Asn	Gly	Ile	Met	Val	Glu	Leu	Pro	Gln	Leu
		435					440					445			
Thr	Ile	His	Gln	Met	Pro	Cys	Lys	Trp	Gly	Trp	Ala	Leu	Ala	Leu	Thr
	450					455					460				

Asn Val Ile
465

<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 196
tggtttgacc aggccaagtt cgg 23

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 197
ggattcatcc tcaaggaaga gcgg 24

<210> 198
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 198
aacttgagc atcagccact ctgc 24

<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 199

ttccgtgccc agcttcggta gcgagtgggt ctgggtggtat tggca

45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

agcagggaaa	tccggatgtc	tcggttatga	agtggagcag	tgagtgtgag	cctcaacata	60
gttccagaac	tctccatccg	gactagttat	tgagcatctg	cctctcatat	caccagtggc	120
catctgaggt	gtttccctgg	ctctgaaggg	gtaggcacga	tggccagggtg	cttcagcctg	180
gtgttgcttc	tcacttccat	ctggaccacg	aggctcctgg	tccaaggctc	tttgctgca	240
gaagagcttt	ccatccaggt	gtcatgcaga	attatgggga	tcacccttgt	gagcaaaaag	300
gcgaaccagc	agctgaattt	cacagaagct	aaggaggcct	gtaggctgct	gggactaagt	360
ttggccggca	aggaccaagt	tgaacagcc	ttgaaagcta	gctttgaaac	ttgcagctat	420
ggctggggtg	gagatggatt	cgtggtcac	tctaggatta	gccccaaacc	caagtgtggg	480
aaaaatgggg	tgggtgtcct	gatttggaag	gttccagtga	gccgacagtt	tgcagcctat	540
tgttacaact	catctgatac	ttggactaac	tcgtgcattc	cagaaattat	caccaccaa	600
gatcccatat	tcaacactca	aactgcaaca	caaacaacag	aatttattgt	cagtgcagct	660
acctactcgg	tggcatcccc	ttactctaca	atacctgccc	ctactactac	tcctcctgct	720
ccagcttcca	cttctattcc	acggagaaaa	aaattgattt	gtgtcacaga	agtttttatg	780
gaaactagca	ccatgtctac	agaaactgaa	ccatttgttg	aaaataaagc	agcattcaag	840
aatgaagctg	ctgggttttg	aggtgtcccc	acggctctgc	tagtgcttgc	tctcctcttc	900
tttggtgctg	cagctgggtc	tggattttgc	tatgtcaaaa	ggtatgtgaa	ggccttccct	960
tttacaacaa	agaatcagca	gaaggaaatg	atcgaaacca	aagtagtaaa	ggaggagaag	1020
gccaatgata	gcaaccctaa	tgaggaatca	aagaaaactg	ataaaaaccc	agaagagtcc	1080
aagagtccaa	gcaaaactac	cgtgcatg	ctggaagctg	aagtttagat	gagacagaaa	1140
tgaggagaca	cacctgaggc	tggtttcttt	catgctcctt	accctgcccc	agctggggaa	1200
atcaaaaggg	ccaaagaacc	aaagaagaaa	gtccaccctt	ggttcctaac	tggaatcagc	1260
tcaggactgc	cattggacta	tggagtgcac	caaagagaat	gcccttctcc	ttattgtaac	1320
cctgtctgga	tcctatcttc	ctacctccaa	agcttcccac	ggcctttcta	gcctggctat	1380
gtcctaataa	tatcccactg	ggagaaagga	gttttgcaaa	gtgcaaggac	ctaaaacatc	1440
tcatcagtat	ccagtggtaa	aaaggcctcc	tggctgtctg	aggctagggtg	ggttgaaagc	1500
caaggagtca	ctgagaccaa	ggctttctct	actgattccg	cagctcagac	cctttcttca	1560
gctctgaaag	agaaacacgt	atcccacctg	acatgtcctt	ctgagcccgg	taagagcaaa	1620
agaatggcag	aaaagtttag	cccctgaaag	ccatggagat	tctcataact	tgagacctaa	1680
tctctgtaaa	gctaaaataa	agaaatagaa	caaggctgag	gatacgacag	tacactgtca	1740
gcagggactg	taaacacaga	caggggtcaaa	gtgttttctc	tgaacacatt	gagttggaat	1800
cactgttttag	aacacacaca	cttacttttt	ctggctctcta	ccactgctga	tattttctct	1860
aggaaatata	cttttacaag	taacaaaaat	aaaaactctt	ataaatttct	atttttatct	1920
gagttacaga	aatgattact	aaggaagatt	actcagtaat	ttgttttaaa	agtaataaaa	1980
ttcaacaaac	atttgctgaa	tagctactat	atgtcaagtg	ctgtgcaagg	tattacactc	2040
tgtaattgaa	tattattcct	caaaaaattg	cacatagtag	aacgctatct	gggaagctat	2100
ttttttcagt	tttgatattt	ctagcttatc	tacttccaaa	ctaattttta	tttttgctga	2160
gactaatctt	attcattttc	tctaatatgg	caaccattat	aaccttaatt	tattattaac	2220
atacctaaga	agtacattgt	tacctctata	taccaagca	catttttaaa	gtgccattaa	2280
caaatgtatc	actagccctc	ctttttccaa	caagaaggga	ctgagagatg	cagaaatatt	2340
tgtgacaaaa	aattaaagca	tttagaaaac	tt			2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr	
1				5				10						15		
Thr	Arg	Leu	Leu	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile	
		20					25						30			
Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala	
		35					40					45				
Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu	
	50					55					60					
Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala	
65					70					75					80	
Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val	
				85					90					95		
Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly	
		100						105					110			
Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys	
		115					120					125				
Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile	
	130					135					140					
Thr	Thr	Lys	Asp	Pro	Ile	Phe	Asn	Thr	Gln	Thr	Ala	Thr	Gln	Thr	Thr	
145					150					155					160	
Glu	Phe	Ile	Val	Ser	Asp	Ser	Thr	Tyr	Ser	Val	Ala	Ser	Pro	Tyr	Ser	
				165					170					175		
Thr	Ile	Pro	Ala	Pro	Thr	Thr	Thr	Pro	Pro	Ala	Pro	Ala	Ser	Thr	Ser	
		180						185					190			
Ile	Pro	Arg	Arg	Lys	Lys	Leu	Ile	Cys	Val	Thr	Glu	Val	Phe	Met	Glu	
		195					200					205				
Thr	Ser	Thr	Met	Ser	Thr	Glu	Thr	Glu	Pro	Phe	Val	Glu	Asn	Lys	Ala	
	210					215					220					
Ala	Phe	Lys	Asn	Glu	Ala	Ala	Gly	Phe	Gly	Gly	Val	Pro	Thr	Ala	Leu	
225					230					235					240	
Leu	Val	Leu	Ala	Leu	Leu	Phe	Phe	Gly	Ala	Ala	Ala	Gly	Leu	Gly	Phe	
				245					250					255		
Cys	Tyr	Val	Lys	Arg	Tyr	Val	Lys	Ala	Phe	Pro	Phe	Thr	Asn	Lys	Asn	
			260					265					270			

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
275 280 285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
290 295 300

Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
305 310 315 320

Glu Val

<210> 202
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202
gagctttcca tccaggtgtc atgc 24

<210> 203
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 203
gtcagtgaca gtacctactc gg 22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 204
tggagcagga ggagtagtag tagg 24

<210> 205
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 205
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206
<211> 1620
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (973)..(973)
<223> a, t, c or g

<220>
<221> modified_base
<222> (977)..(977)
<223> a, t, c or g

<220>
<221> modified_base
<222> (996)..(996)
<223> a, t, c or g

<220>
<221> modified_base
<222> (1003)..(1003)
<223> a, t, c or g

<400> 206
agatggcggg cttggcacct ctaattgctc tcgtgtattc ggtgccgga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgtcttc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggg aaccctgtgtg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttggata ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaaccac ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagaggggc acttggattg 480
tggagtctct tgccaattgg tctaattgact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acaggggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagtgtgca catcacccct caccaagcaa ctccctaccc 660
tgatcctgtt ccaagggtggc aaggaggcaa tgccggcgcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gagcagcctg 840
tggcttcaac cccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttctctt cctgtcaatt ccaggtctct tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcaccc tacaggaagg cctgccatgc 1080
tgtggccaac tgtttactg gagcaagaaa gagatctcat aggacggagg gggaaatggg 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccctaa gcccttctgg ctctgcttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttgaggga gaaatccctt ggactttcac taaccctctg 1560
acatactccc cacaccagtt tgatggcttt ccgtaataaa aagattggga tttccttttt 1620

<210> 207
<211> 296
<212> PRT
<213> Homo sapiens

<400> 207

Met	Ala	Val	Leu	Ala	Pro	Leu	Ile	Ala	Leu	Val	Tyr	Ser	Val	Pro	Arg	
1				5					10					15		
Leu	Ser	Arg	Trp	Leu	Ala	Gln	Pro	Tyr	Tyr	Leu	Leu	Ser	Ala	Leu	Leu	
			20					25					30			
Ser	Ala	Ala	Phe	Leu	Leu	Val	Arg	Lys	Leu	Pro	Pro	Leu	Cys	His	Gly	
			35				40					45				
Leu	Pro	Thr	Gln	Arg	Glu	Asp	Gly	Asn	Pro	Cys	Asp	Phe	Asp	Trp	Arg	
	50					55					60					
Glu	Val	Glu	Ile	Leu	Met	Phe	Leu	Ser	Ala	Ile	Val	Met	Met	Lys	Asn	
65					70					75					80	
Arg	Arg	Ser	Ile	Thr	Val	Glu	Gln	His	Ile	Gly	Asn	Ile	Phe	Met	Phe	
				85					90					95		
Ser	Lys	Val	Ala	Asn	Thr	Ile	Leu	Phe	Phe	Arg	Leu	Asp	Ile	Arg	Met	
			100					105					110			
Gly	Leu	Leu	Tyr	Ile	Thr	Leu	Cys	Ile	Val	Phe	Leu	Met	Thr	Cys	Lys	
		115					120					125				
Pro	Pro	Leu	Tyr	Met	Gly	Pro	Glu	Tyr	Ile	Lys	Tyr	Phe	Asn	Asp	Lys	
		130				135					140					
Thr	Ile	Asp	Glu	Glu	Leu	Glu	Arg	Asp	Lys	Arg	Val	Thr	Trp	Ile	Val	
145					150					155					160	
Glu	Phe	Phe	Ala	Asn	Trp	Ser	Asn	Asp	Cys	Gln	Ser	Phe	Ala	Pro	Ile	
				165					170					175		
Tyr	Ala	Asp	Leu	Ser	Leu	Lys	Tyr	Asn	Cys	Thr	Gly	Leu	Asn	Phe	Gly	
			180					185					190			
Lys	Val	Asp	Val	Gly	Arg	Tyr	Thr	Asp	Val	Ser	Thr	Arg	Tyr	Lys	Val	
		195					200					205				
Ser	Thr	Ser	Pro	Leu	Thr	Lys	Gln	Leu	Pro	Thr	Leu	Ile	Leu	Phe	Gln	
	210					215					220					
Gly	Gly	Lys	Glu	Ala	Met	Arg	Arg	Pro	Gln	Ile	Asp	Lys	Lys	Gly	Arg	
225					230					235					240	
Ala	Val	Ser	Trp	Thr	Phe	Ser	Glu	Glu	Asn	Val	Ile	Arg	Glu	Phe	Asn	
				245					250					255		
Leu	Asn	Glu	Leu	Tyr	Gln	Arg	Ala	Lys	Lys	Leu	Ser	Lys	Ala	Gly	Asp	
			260					265					270			

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
290 295

<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 208
gcttgatattcgcatgggctac 24

<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 209
tggagacaatatccctgagg 20

<210> 210
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 210
aacagttggcacagcatggcagg 24

<210> 211
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 211
ccattgatgaggaaactagaaagggaagaagggtcacttgattgtggag 50

<210> 212
<211> 1985

<212> DNA
<213> Homo sapiens

<400> 212

```
ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60
tggggccccca gcctggcccc gggtaccctg gcatgaggag atgggcctgt tgctcctggt 120
cccattgctc ctgctgcccc gctcctacgg actgcccttc tacaacggct tctactactc 180
caacagcgcc aacgaccaga acctaggcaa cgggtcatggc aaagacctcc ttaatggagt 240
gaagctgggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300
cctgccctgc cgctaccgct acgagccggc cctggctctcc ccgcggcgtg tgcgtgtcaa 360
atgggtggaag ctgtcggaga acggggcccc agagaaggac gtgctgggtg ccatcgggct 420
gaggcaccgc tcctttgggg actaccaagg ccgctgtcac ctgcggcagg acaaagagca 480
tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540
ggtcattgac gggctggagg atgaaagcgg tctgggtggag ctggagctgc ggggtgtggt 600
ctttccttac cagtccccca acgggcgcta ccagttcaac ttccacgagg gccagcaggt 660
ctgtgcagag caggctgcgg tgggtggcctc ctttgagcag ctcttcgggg cctgggagga 720
gggcctggac tgggtgcaacg cgggctgggt gcaggatgct acggtgcagt accccatcat 780
gttgcccccg cagccctgcg gtggcccagg cctggcacct ggcgtgcgaa gctacggccc 840
ccgccaccgc cgctgcacc gctatgatgt attctgtctc gctactgcc tcaaggggcg 900
ggtgtactac ctggagcacc ctgagaagct gacgtgaca gaggcaaggg aggcctgcc 960
ggaagatgat gccacgatcg ccaagggtgg acagctcttt gccgcctgga agttccatgg 1020
cctggaccgc tgcgacgtg gctggctggc agatggcagc gtccgctacc ctgtggttca 1080
cccgatcctt aactgtgggc cccagagcc tgggggtccga agctttggct tccccgacct 1140
gcagagccgc ttgtacggtg tttactgcta ccgccagcac taggacctgg ggccctcccc 1200
tgccgcattc cctcactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttgg 1260
agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacad ttttttacta 1320
ttttttgtaa agcaaacaga acccaatgcc tccctttgct cctggatgcc cactccagg 1380
aatcatgctt gctcccctgg gccatttgcg gttttgtggg cttctggagg gttccccgcc 1440
atccaggctg gtctccctcc cttaaggagg ttggtgcca gagtgggcgg tggcctgtct 1500
agaatgccgc cgggagtcgc ggcattgggt gcacagttct ccctgcccct cagcctgggg 1560
gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctcctg cccacctcta 1620
cttctctgtg aagccgctga cccagctctg cccactgagg ggctagggct ggaagccagt 1680
tctaggcttc caggcgaat ctgaggaag gaagaaactc ccctccccgt tccccttccc 1740
ctctcggttc caaagaatct gttttgttgt catttgtttc tcctgtttcc ctgtgtgggg 1800
aggggcccctc aggtgtgtgt actttggaca ataaatgggt ctatgactgc cttccgccaa 1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaa                                             1985
```

<210> 213
<211> 360
<212> PRT
<213> Homo sapiens

<400> 213

```
Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
  1                      5                      10                      15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
  20                      25                      30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
  35                      40                      45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
  50                      55                      60
```

Ser	Val	Ile	Leu	Pro	Cys	Arg	Tyr	Arg	Tyr	Glu	Pro	Ala	Leu	Val	Ser	65	70	75	80
Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	Leu	Ser	Glu	Asn	Gly	Ala	85	90	95	
Pro	Glu	Lys	Asp	Val	Leu	Val	Ala	Ile	Gly	Leu	Arg	His	Arg	Ser	Phe	100	105	110	
Gly	Asp	Tyr	Gln	Gly	Arg	Val	His	Leu	Arg	Gln	Asp	Lys	Glu	His	Asp	115	120	125	
Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr	130	135	140	
Arg	Cys	Glu	Val	Ile	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu	145	150	155	160
Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg	165	170	175	
Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala	180	185	190	
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly	195	200	205	
Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr	210	215	220	
Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Gly	Leu	Ala	Pro	225	230	235	240
Gly	Val	Arg	Ser	Tyr	Gly	Pro	Arg	His	Arg	Arg	Leu	His	Arg	Tyr	Asp	245	250	255	
Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Lys	Gly	Arg	Val	Tyr	Tyr	Leu	Glu	260	265	270	
His	Pro	Glu	Lys	Leu	Thr	Leu	Thr	Glu	Ala	Arg	Glu	Ala	Cys	Gln	Glu	275	280	285	
Asp	Asp	Ala	Thr	Ile	Ala	Lys	Val	Gly	Gln	Leu	Phe	Ala	Ala	Trp	Lys	290	295	300	
Phe	His	Gly	Leu	Asp	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser	305	310	315	320
Val	Arg	Tyr	Pro	Val	Val	His	Pro	His	Pro	Asn	Cys	Gly	Pro	Pro	Glu	325	330	335	
Pro	Gly	Val	Arg	Ser	Phe	Gly	Phe	Pro	Asp	Pro	Gln	Ser	Arg	Leu	Tyr	340	345	350	
Gly	Val	Tyr	Cys	Tyr	Arg	Gln	His									355	360		

<210> 214
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 214
 tgcttcgcta ctgccctc 18

 <210> 215
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 215
 ttcccttggtg ggttgagg 18

 <210> 216
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 216
 agggctggaa gccagttc 18

 <210> 217
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 217
 agccagtggag gaaatgag 18

 <210> 218
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 218
tgtccaaagt acacacacct gagg 24

<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 219
gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 220
ggagagcgga gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60
gcttctgttg ctactgaggc acggggccca ggggaagcca tccccagacg caggccctca 120
tgggcagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcca 180
cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240
ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300
cgcgggggac ggcgacggct ggggtgtcgt ggccgagctt cgcgcggtga tcgcgcacac 360
gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420
cgacgggcgt gtgggttggg aggagctgag caacgccacc tatggccact acgcgcccgg 480
tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540
gcggcggttt cggttgggcg accaggatgg ggactcgatg gccactcgag aggagctgac 600
agccttcctg caccctgagg agttccctca catgcgggac atcgtgattg ctgaaaccct 660
ggaggacctg gacagaaaca aagatggcta tgtccagggtg gaggagtaca tcgcggatct 720
gtactcagcc gagcctgggg aggaggagcc ggcggtgggtg cagacggaga ggcagcagtt 780
ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggcccactg 840
ggtgctgccc cctgcccagg accagcccct ggtggaagcc aaccacctgc tgcacgagag 900
cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960
tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020
agcaccgcgc acctgccaca gcctcagagg cccgcacaat gaccggagga ggggcccgtg 1080
tggtctggcc cctcctctgt ccaggccccg caggaggcag atgcagtccc aggcattctc 1140
ctgcccctgg gctctcaggg accccttggg tcggcttctg tccctgtcac accccaacc 1200
ccagggaggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260
cagcccagac ccagggaccc ttggcccca gctcagctct aagaaccgcc ccaaccctc 1320
cagctccaaa tctgagcctc caccacatag actgaaactc cctggcccc agccctctcc 1380
tgcttggcct ggcttgggac acctctctc tgccaggagg caataaaagc cagcgccggg 1440
accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaa 1503

<210> 221
<211> 328
<212> PRT
<213> Homo sapiens

<400> 221
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His
1 5 10 15

Gly	Ala	Gln	Gly	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly	20	25	30
Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala	35	40	45
His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu	Val	50	55	60
Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu	65	70	75
Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp	85	90	95
Val	Ser	Leu	Ala	Glu	Leu	Arg	Ala	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg	100	105	110
His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp	115	120	125
Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn	Ala	Thr	Tyr	Gly	130	135	140
His	Tyr	Ala	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr	145	150	155
Tyr	Lys	Lys	Met	Leu	Ala	Arg	Asp	Glu	Arg	Arg	Phe	Arg	Val	Ala	Asp	165	170	175
Gln	Asp	Gly	Asp	Ser	Met	Ala	Thr	Arg	Glu	Glu	Leu	Thr	Ala	Phe	Leu	180	185	190
His	Pro	Glu	Glu	Phe	Pro	His	Met	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr	195	200	205
Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	Gln	Val	Glu	Glu	210	215	220
Tyr	Ile	Ala	Asp	Leu	Tyr	Ser	Ala	Glu	Pro	Gly	Glu	Glu	Glu	Pro	Ala	225	230	235
Trp	Val	Gln	Thr	Glu	Arg	Gln	Gln	Phe	Arg	Asp	Phe	Arg	Asp	Leu	Asn	245	250	255
Lys	Asp	Gly	His	Leu	Asp	Gly	Ser	Glu	Val	Gly	His	Trp	Val	Leu	Pro	260	265	270
Pro	Ala	Gln	Asp	Gln	Pro	Leu	Val	Glu	Ala	Asn	His	Leu	Leu	His	Glu	275	280	285
Ser	Asp	Thr	Asp	Lys	Asp	Gly	Arg	Leu	Ser	Lys	Ala	Glu	Ile	Leu	Gly	290	295	300
Asn	Trp	Asn	Met	Phe	Val	Gly	Ser	Gln	Ala	Thr	Asn	Tyr	Gly	Glu	Asp	305	310	315
																		320

Leu Thr Arg His His Asp Glu Leu
325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 225

ccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 226

```

ggggccttgc cttccgcact cgggcgcagc cgggtggatc tcgagcaggt gcggagcccc 60
gggcggcggg cgcggtgctg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120
ccagcctgtc tgtcgctggt ttggcgcccc cgctcccccg cgggtgcgggg ttgcacaccg 180
atcctgggct tcgctcgatt tgccgcccag gcgcctccca gacctagagg ggcgctggcc 240
tgagcagcgc ggtcgctctgt gtctctcttc ctctgcgcgc cgcccgggga tccgaagggg 300
gcggggctct gaggaggtga cgcgcggggc ctcccgacc ctggccttgc ccgcattctc 360
cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atccccgctc 420
tcggcctcgg tgtgtgtctg ctgtgtgtgc cggggcccg gcgcagcag ggagccgctc 480
ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540
tctgcccagg gggctgccct cttgaggaat tctctgtgta tgggaacata gtatatgtct 600
ctgtatcgag catatgtggg gctgtgttcc acaggggagt aatcagcaac tcagggggac 660
ctgtacgagt ctatagccta cctggtcgag aaaactattc ctcagtagat gccaatggca 720
tccagtctca aatgctttct agatggctct cttctttcac agtaactaaa ggcaaaagta 780
gtacacagga ggccacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgac 840
taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900
tgattgatgg aagctttaat attgggcagc gccgatttaa ttacagaag aattttgttg 960
gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020
ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080
tgtttgccat aaaggaagta ggtttcagag ggggtaattc caatacagga aaagccttag 1140
agcatactgc tcagaaattc ttcacggtag atgtctggag aagaaaaggg atccccaaag 1200
tggtggtggt atttattgat ggttggcctt ctgatgacat cgaggaagca ggcattgttg 1260
ccagagagtt tgggtgtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320
tggggatggt tcaggatgtc acatttgttg acaaggctgt ctgtcggaat aatggcttct 1380
tctcttacca catgccaac tggtttgcca ccacaaaata cgtaaagcct ctggtacaga 1440
agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1500
ccttttctaat tgatggctcc agcagtgttg gagatagcaa tttccgcctc atgcttgaat 1560
ttgtttccaa catagccaag acttttgaaa tctcggacat tggtgccaag atagctgctg 1620
tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1680
atgtcctagc tgtcatcaga aacatccgct atatgagtgg tggaacagct actggtgatg 1740
ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800
tcctagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860
cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920
tgaaagatat ggcttctaaa ccgaaggagt ctacgcctt cttcacaaga gagttcacag 1980
gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040
agcaataatg gtaacatttt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100
attgtattct cataactctg aaatgcttta gcatactaga atcagataca aaactattaa 2160
gtatgtcaac agccatttag gcaaataagc actcctttaa agccgctgcc ttctggttac 2220
aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataatcatgg ctcttagaaa 2280
ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340
tgtacagata tgcaaattcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaaa 2400
aaa
2403

```

<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

```

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
  1              5              10              15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
          20          25          30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
          35          40          45

```

Leu	Cys	Pro	Gly	Gly	Cys	Pro	Leu	Glu	Glu	Phe	Ser	Val	Tyr	Gly	Asn		
50						55					60						
Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg		
65					70					75					80		
Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro		
				85					90					95			
Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln		
			100					105					110				
Met	Leu	Ser	Arg	Trp	Ser	Ala	Ser	Phe	Thr	Val	Thr	Lys	Gly	Lys	Ser		
		115					120					125					
Ser	Thr	Gln	Glu	Ala	Thr	Gly	Gln	Ala	Val	Ser	Thr	Ala	His	Pro	Pro		
	130					135					140						
Thr	Gly	Lys	Arg	Leu	Lys	Lys	Thr	Pro	Glu	Lys	Lys	Thr	Gly	Asn	Lys		
145					150					155					160		
Asp	Cys	Lys	Ala	Asp	Ile	Ala	Phe	Leu	Ile	Asp	Gly	Ser	Phe	Asn	Ile		
				165					170					175			
Gly	Gln	Arg	Arg	Phe	Asn	Leu	Gln	Lys	Asn	Phe	Val	Gly	Lys	Val	Ala		
			180					185					190				
Leu	Met	Leu	Gly	Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln		
	195						200					205					
Ala	Ser	Glu	His	Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser		
	210					215					220						
Ala	Lys	Asp	Val	Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly		
225					230					235					240		
Asn	Ser	Asn	Thr	Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe		
				245					250					255			
Thr	Val	Asp	Ala	Gly	Val	Arg	Lys	Gly	Ile	Pro	Lys	Val	Val	Val	Val		
			260					265					270				
Phe	Ile	Asp	Gly	Trp	Pro	Ser	Asp	Asp	Ile	Glu	Glu	Ala	Gly	Ile	Val		
	275						280					285					
Ala	Arg	Glu	Phe	Gly	Val	Asn	Val	Phe	Ile	Val	Ser	Val	Ala	Lys	Pro		
	290					295					300						
Ile	Pro	Glu	Glu	Leu	Gly	Met	Val	Gln	Asp	Val	Thr	Phe	Val	Asp	Lys		
305					310					315					320		
Ala	Val	Cys	Arg	Asn	Asn	Gly	Phe	Phe	Ser	Tyr	His	Met	Pro	Asn	Trp		
				325					330					335			
Phe	Gly	Thr	Thr	Lys	Tyr	Val	Lys	Pro	Leu	Val	Gln	Lys	Leu	Cys	Thr		
			340					345					350				

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
 385 390 395 400
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
 515 520 525
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
 530 535 540
 Phe Leu Glu Ser Gln Gln
 545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229

ctgctgtcca caggggag

18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230

ccttgaagca tactgctc

18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231

gagatagcaa tttccgcc

18

<210> 232

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 232

ttcctcaaga gggcagcc

18

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 233

cttggcacca atgtccgaga tttc

24

<210> 234

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 234

gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

cgccgcgctc	ccgcacccgc	ggccccccca	ccgcgcgcgt	cccgcacctg	cacccgcagc	60
ccggcggcct	cccggcggga	gcgagcagat	ccagtcgggc	ccgcagcgca	actcgggtcca	120
gtcggggcgg	cggctgcggg	cgcagagcgg	agatgcagcg	gcttggggcc	accctgctgt	180
gcctgctgct	ggcggcgccg	gtccccacgg	ccccgcgcgc	cgctccgacg	gcgacctcgg	240
ctccagctcaa	gcccggcccc	gctctcagct	accgcgagga	ggaggccacc	ctcaatgaga	300
tgttccgcga	ggttgaggaa	ctgatggagg	acacgcagca	caaattgcgc	agcgcggtgg	360
aagagatgga	ggcagaagaa	gctgctgcta	aagcatcatc	agaagtgaac	ctggcaaact	420
tacctccag	ctatcacaat	gagaccaaca	cagacacgaa	ggttggaat	aataccatcc	480
atgtgcaccg	agaaattcac	aagataacca	acaaccagac	tggacaaatg	gtcttttcag	540
agacagttaa	cacatctgtg	ggagacgaag	aaggcagaag	gagccacgag	tgcacatcgc	600
acgaggactg	tggggccagc	atgtactgcc	agtttgccag	cttcacgtac	acctgccagc	660
catgccgggg	ccagaggatg	ctctgcaccc	gggacagtga	gtgctgtgga	gaccagctgt	720
gtgtctgggg	tactgcacc	aaaatggcca	ccaggggcag	caatgggacc	atctgtgaca	780
accagaggga	ctgccagccg	gggctgtgct	gtgccttcca	gagaggcctg	ctgttcctctg	840
tgtgcacacc	cctgcccgtg	gagggcgagc	tttgccatga	ccccgccagc	cggcttcttg	900
acctcatcac	ctgggagcta	gagcctgatg	gagccttgga	ccgatgccct	tgtgccagtg	960
gcctcctctg	ccagccccac	agccacagcc	tggtgtatgt	gtgcaagccg	accttcgttg	1020
ggagccgtga	ccaagatggg	gagatcctgc	tgcccagaga	ggtccccgat	gagtatgaag	1080
ttggcagctt	catggaggag	gtgcgccagg	agctggagga	cctggagagg	agcctgactg	1140
aagagatggc	gctgggggag	cctgcggctg	ccgccgctgc	actgctggga	ggggaagaga	1200
tttagatctg	gaccaggctg	tgggtagatg	tgcaatagaa	atagctaatt	tatttcccca	1260
ggtgtgtgct	ttaggcgtgg	gctgaccagg	cttcttccca	catcttcttc	ccagtaagtt	1320
tcccctcttg	cttgacagca	tgaggtgttg	tgcatttggt	cagctcccc	aggctgttct	1380
ccaggcttca	cagcttggtg	cttgggagag	tcaggcaggg	ttaaactgca	ggagcagttt	1440
gccacccctg	tcagatttat	tggctgcttt	gcctctacca	gttggcagac	agccgtttgt	1500
tctacatggc	tttgataatt	gtttgagggg	aggagatgga	aacaatgtgg	agtctccctc	1560
tgattggttt	tggggaaatg	tggagaagag	tgccctgctt	tgcaaaccatc	aacctggcaa	1620
aaatgcaaca	aatgaatttt	ccacgcagtt	ctttccatgg	gcataggtaa	gctgtgcctt	1680
cagctgttgc	agatgaaatg	ttctgttcac	cctgcattac	atgtgtttat	tcacccagca	1740
gtgttgctca	gctcctacct	ctgtgccagg	gcagcatttt	catatccaag	atcaattccc	1800
tctctcagca	cagcctgggg	aggggggtcat	tgttctcctc	gtccatcagg	gatctcagag	1860
gctcagagac	tgcaagctgc	ttgcccgaag	cacacagcta	gtgaagacca	gagcagtttc	1920
atctggttgt	gactctaagc	tcagtgtctc	ctccactacc	ccacaccagc	cttgggtgcca	1980
ccaaaagtgc	tccccaaaag	gaaggagaat	gggatttttc	ttgaggcatg	cacatctgga	2040
attaaggtca	aactaattct	cacatccctc	taaaagtaaa	ctactgttag	gaacagcagt	2100
gttctcacag	tgtggggcag	ccgtccttct	aatgaagaca	atgatattga	actgtccct	2160
ctttggcagt	tgcattagta	actttgaaag	gtatatgact	gagcgtagca	tacagggttaa	2220
cctgcagaaa	cagtacttag	gtaattgtag	ggcgaggatt	ataaatgaaa	tttgcaaaat	2280
cacttagcag	caactgaaga	caattatcaa	ccacgtggag	aaaatcaaac	cgagcagggc	2340
tgtgtgaaac	atggttgtaa	tatgcgactg	cgaacactga	actctacgcc	actccacaaa	2400
tgatgttttc	aggtgtcatg	gactgttgcc	accatgtatt	catccagagt	tcttaaagtt	2460
taaagttgca	catgattgta	taagcatgct	ttctttgagt	tttaaattat	gtataaacat	2520

aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
aaaaaa 2586

<210> 236
<211> 350
<212> PRT
<213> Homo sapiens

<400> 236
Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
1 5 10 15
Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
20 25 30
Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95
Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
100 105 110
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 120 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
325 330 335

Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
340 345 350

<210> 237

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

ggagctgcac cccttgc

17

<210> 238

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 238

ggaggactgt gccacatga gagactcttc aaaccaagg caaaattgg

49

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 239

gcagagcggg gatgcagcgg cttg

24

<210> 240

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 240

ttggcagctt catggagg

18

<210> 241

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 241

cctgggcaaa aatgcaac

18

<210> 242

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 242

ctccagctcc tggcgcacct cctc

24

<210> 243

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 243

ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg

45

<210> 244

<211> 3679

<212> DNA

<213> Homo Sapien

<400> 244

aaggaggctg ggaggaaaga ggtaagaaag gtagagaaac ctacctcaca 50

tctctctggg ctcaagaaga ctctgaagat aacaataatt tcagcccatc 100

cactctcctt ccttcccaaa cacacatgtg catgtacaca cacacataca 150

cacacataca ctttctcttc cttcactgaa gactcacagt cactcactct 200

gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcttgagg 250

attacctctg cagctccttt ggcttggtga gtcaaaaaac atgggagggg 300

ccaggcacgg tgactcacac ctgtaatccc agcatttttg gagaccgagg 350

tgagcagatc acttgaggtc aggagttcga gaccagcctg gccaacatgg 400
agaaaccccc atctctacta aaaatacaaa aattagccag gagtgggtggc 450
aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500
gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550
gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600
ggggtagata ctgcttctct gcaacctcct taactctgca tcctcttctt 650
ccagggctgc ccctgatggg gcctggcaat gactgagcag gccagcccc 700
agaggacaag gaagagaagg catattgagg agggcaagaa gtgacgcccg 750
gtgtagaatg actgccttg gaggggtggtt ccttggggccc tggcagggtt 800
gctgaccctt accctgcaaa acacaaagag caggactcca gactctcctt 850
gtgaatggtc ccctgccctg cagctccacc atgaggcttc tcgtggcccc 900
actcttgcta gcttgggtgg ctggtgccac tgccactgtg cccgtggtac 950
cctggcatgt tcctgcccc cctcagtgtg cctgccagat ccggccctgg 1000
tatacgcctt gctcgtccta ccgcgaggct accactgtgg actgcaatga 1050
cctattcctg acggcagtc ccccggcact ccccgcaggc acacagacct 1100
tgctcctgca gagcaacagc attgtccgtg tggaccagag tgagctgggc 1150
tacctggcca atctcacaga gctggacctg tcccagaaca gcttttcgga 1200
tgcccagac tgtgatttcc atgccctgcc ccagctgctg agcctgcacc 1250
tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggtg 1300
gccagcctac aggaactcta tctcaaccac aaccagctct accgcatcgc 1350
ccccagggcc ttttctggcc tcagcaactt gctgcggctg cacctcaact 1400
ccaacctcct gagggccatt gacagccgct ggtttgaaat gctgccaac 1450
ttggagatac tcatgattgg cggcaacaag gtagatgcca tcctggacat 1500
gaacttccgg ccctggcca acctgcgtag cctggtgcta gcaggcatga 1550
acctgcggga gatctccgac tatgccttg aggggctgca aagcctggag 1600
agcctctcct tctatgaaa ccagctggcc cgggtgcca ggcgggcact 1650
ggaacaggtg cccgggtca agttcctaga cctcaacaag aaccgctcc 1700
agcgggtagg gccgggggac tttgccaaca tgctgcacct taaggagctg 1750

ggactgaaca acatggagga gctgggtctcc atcgacaagt ttgccctggt 1800
gaacctcccc gagctgacca agctggacat caccaataac ccacggctgt 1850
ccttcatecca cccccgcgcc ttccaccacc tgccccagat ggagaccctc 1900
atgctcaaca acaacgctct cagtgccttg caccagcaga cgggtggagtc 1950
cctgccaac ctgcaggagg taggtctcca cggcaacccc atccgctgtg 2000
actgtgtcat ccgctggggc aatgccacgg gcacccgtgt ccgcttcac 2050
gagccgcaat ccaccctgtg tgcggagcct ccggacctcc agcgcctccc 2100
ggtccgtgag gtgcccttcc gggagatgac ggaccactgt ttgccctca 2150
tctccccacg aagcttcccc ccaagcctcc aggtagccag tggagagagc 2200
atggtgctgc attgccgggc actggccgaa cccgaacccg agatctactg 2250
ggtcactcca gctgggcttc gactgacacc tgcccatgca ggcaggaggt 2300
accgggtgta ccccgagggg accctggagc tgcggagggg gacagcagaa 2350
gaggcagggc tatacacctg tgtggcccag aacctggtgg gggctgacac 2400
taagacggtt agtgtggtt tgggccgtgc tctcctccag ccaggcaggg 2450
acgaaggaca ggggctggag ctccgggtgc aggagacca ccctatcac 2500
atcctgctat cttgggtcac cccaccaac acagtgtcca ccaacctcac 2550
ctggtccagt gcctcctccc tccggggcca gggggccaca gctctggccc 2600
gcctgcctcg gggaaccac agctacaaca ttaccgcct ccttcaggcc 2650
acggagtact gggcctgcct gcaagtggcc tttgctgatg cccacacca 2700
gttggttgt gtatgggcca ggaccaaaga ggccacttct tgccacagag 2750
ccttagggga tcgtcctggg ctcatgcca tcctggctct cgctgtcctt 2800
ctcctggcag ctgggctagc ggcccacctt ggcacaggcc aaccaggaa 2850
gggtgtgggt gggaggcggc ctctccctcc agcctgggct ttctggggct 2900
ggagtgcctt ttctgtccgg gttgtgtctg ctcccctcgt cctgccctgg 2950
aatccaggga ggaagctgcc cagatcctca gaaggggaga cactgttgcc 3000
accattgtct caaaattctt gaagctcagc ctgttctcag cagtagagaa 3050
atcactagga ctacttttta ccaaaagaga agcagtctgg gccagatgcc 3100
ctgccaggaa agggacatgg acccacgtgc ttgaggcctg gcagctgggc 3150
caagacagat ggggctttgt ggcctgggg gtgcttctgc agccttgaaa 3200

aagttgccct tacctcctag ggtcacctct gctgccattc tgaggaacat 3250
ctccaaggaa caggaggagac tttggctaga gcctcctgcc tccccatctt 3300
ctctctgccc agaggctcct gggcctggct tggctgtccc ctacctgtgt 3350
ccccgggctg cacccttcc tcttctcttt ctctgtacag tctcagttgc 3400
ttgctcttgt gcctcctggg caagggtga aggaggccac tccatctcac 3450
ctcggggggc tgccctcaat gtgggagtga cccagccag atctgaagga 3500
catttgggag agggatgccc aggaacgcct catctcagca gcctgggctc 3550
ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600
atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650
aataaaaata aataataaca ataaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly
1				5					10					15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro
				20					25					30
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
				35					40					45
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
				50					55					60
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
				65					70					75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
				80					85					90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
				95					100					105
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
				110					115					120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
				125					130					135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
				140					145					150

Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	
				155					160					165	
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	
				170					175					180	
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	
				185					190					195	
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	
				200					205					210	
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	
				215					220					225	
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	
				230					235					240	
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	
				245					250					255	
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	
				260					265					270	
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	
				275					280					285	
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	
				290					295					300	
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	
				305					310					315	
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	
				320					325					330	
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	
				335					340					345	
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	
				350					355					360	
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	
				365					370					375	
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	
				380					385					390	
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	
				395					400					405	
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys	
				410					415					420	
Leu	Pro	Leu	Ile	Ser	Pro	Arg	Ser	Phe	Pro	Pro	Ser	Leu	Gln	Val	
				425					430					435	

Ala Ser Gly Glu	Ser Met Val Leu His	Cys Arg Ala Leu Ala Glu
440	445	450
Pro Glu Pro Glu	Ile Tyr Trp Val Thr	Pro Ala Gly Leu Arg Leu
455	460	465
Thr Pro Ala His	Ala Gly Arg Arg Tyr	Arg Val Tyr Pro Glu Gly
470	475	480
Thr Leu Glu Leu	Arg Arg Val Thr Ala	Glu Glu Ala Gly Leu Tyr
485	490	495
Thr Cys Val Ala	Gln Asn Leu Val Gly	Ala Asp Thr Lys Thr Val
500	505	510
Ser Val Val Val	Gly Arg Ala Leu Leu	Gln Pro Gly Arg Asp Glu
515	520	525
Gly Gln Gly Leu	Glu Leu Arg Val Gln	Glu Thr His Pro Tyr His
530	535	540
Ile Leu Leu Ser	Trp Val Thr Pro Pro	Asn Thr Val Ser Thr Asn
545	550	555
Leu Thr Trp Ser	Ser Ala Ser Ser Leu	Arg Gly Gln Gly Ala Thr
560	565	570
Ala Leu Ala Arg	Leu Pro Arg Gly Thr	His Ser Tyr Asn Ile Thr
575	580	585
Arg Leu Leu Gln	Ala Thr Glu Tyr Trp	Ala Cys Leu Gln Val Ala
590	595	600
Phe Ala Asp Ala	His Thr Gln Leu Ala	Cys Val Trp Ala Arg Thr
605	610	615
Lys Glu Ala Thr	Ser Cys His Arg Ala	Leu Gly Asp Arg Pro Gly
620	625	630
Leu Ile Ala Ile	Leu Ala Leu Ala Val	Leu Leu Leu Ala Ala Gly
635	640	645
Leu Ala Ala His	Leu Gly Thr Gly Gln	Pro Arg Lys Gly Val Gly
650	655	660
Gly Arg Arg Pro	Leu Pro Pro Ala Trp	Ala Phe Trp Gly Trp Ser
665	670	675
Ala Pro Ser Val	Arg Val Val Ser Ala	Pro Leu Val Leu Pro Trp
680	685	690
Asn Pro Gly Arg	Lys Leu Pro Arg Ser	Ser Glu Gly Glu Thr Leu
695	700	705
Leu Pro Pro Leu	Ser Gln Asn Ser	
710		

<210> 246
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 246
aacaaggtaa gatgcatcc tg 22

<210> 247
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 247
aaacttgatc atggagacca gctc 24

<210> 248
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 248
aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249
<211> 3401
<212> DNA
<213> Homo Sapien

<400> 249
gcaagccaag gcgctgtttg agaagggtgaa gaagttccgg acccatgtgg 50
aggaggggga catttgtgtac cgcctctaca tgcggcagac catcatcaag 100
gtgatcaagt tcctcctcat catctgtctac accgtctact acgtgcacaa 150
catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200
accgcaccta ccgctgtgcc caccctctgg ccacactctt caagatcctg 250
gcgtccttct acatcagcct agtcatcttc tacggcctca tctgcatgta 300
cacactgtgg tggatgtctac ggcgctccct caagaagtac tcgtttgagt 350
cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400
ttcgccttca tgctgcacct cattgaccaa tacgaccgcg tctactccaa 450

gcgcttcgcc gtcttcctgt cggaggtgag tgagaacaag ctgcggcagc 500
tgaacctcaa caacgagtgg acgctggaca agctccggca gcggctcacc 550
aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600
ccctgacact gtgtttgacc tgggtggagct ggaggtcctc aagctggagc 650
tgatccccga cgtgaccatc ccgcccagca ttgccagct cacgggcctc 700
aaggagctgt ggctctacca cacagcggcc aagattgaag cgctgcgct 750
ggccttcctg cgcgagaacc tgcgggcgct gcacatcaag ttcaccgaca 800
tcaaggagat cccgctgtgg atctatagcc tgaagacact ggaggagctg 850
cacctgacgg gcaacctgag cgcggagaac aaccgctaca tcgtcatcga 900
cgggctgcgg gagctcaaac gcctcaaggt gctgcggctc aagagcaacc 950
taagcaagct gccacaggtg gtcacagatg tgggcgtgca cctgcagaag 1000
ctgtccatca acaatgaggg caccaagctc atcgtcctca acagcctcaa 1050
gaagatggcg aacctgactg agctggagct gatccgctgc gacctggagc 1100
gcatccccca ctccatcttc agcctccaca acctgcagga gattgacctc 1150
aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200
gcaccgcctc acctgcctta agctgtggta caaccacatc gcctacatcc 1250
ccatccagat cggcaacctc accaacctgg agcgcctcta cctgaaccgc 1300
aacaagatcg agaagatccc caccagctc ttctactgcc gcaagctgcg 1350
ctacctggac ctgagccaca acaacctgac cttcctccct gccgacatcg 1400
gcctcctgca gaacctccag aacctagcca tcacggccaa ccg gatcgag 1450
acgctccctc cggagctctt ccagtgccgg aagctgcggg ccctgcacct 1500
gggcaacaac gtgctgcagt cactgccctc caggggtgggc gagctgacca 1550
acctgacgca gatcgagctg cggggcaacc ggctggagtg cctgcctgtg 1600
gagctgggcg agtgcccact gctcaagcgc agcggcttgg tgggtggagga 1650
ggacctgttc aacacactgc caccgaggt gaaggagcgg ctgtggaggg 1700
ctgacaagga gcaggcctga gcgaggccgg cccagcacag caagcagcag 1750
gaccgctgcc cagtctcag gcccgagggg gcaggcctag cttctcccag 1800
aactcccga cagccaggac agcctcgcgg ctgggcagga gcctggggcc 1850
gcttgtgagt caggccagag cgagaggaca gtatctgtgg ggctggcccc 1900

ttttctccct ctgagactca cgtccccag ggcaagtgt tgtggaggag 1950
agcaagtctc aagagcgag tatttggata atcaggggtc cctccctgga 2000
ggccagctct gccccaggg ctgagctgcc accagaggtc ctgggaccct 2050
cactttagtt cttgggtattt atttttctcc atctcccacc tccttcatcc 2100
agataactta tacattccca agaaagttca gccagatgg aaggtgttca 2150
gggaaaggtg ggctgccttt tcccctgtc cttatttagc gatgccgccc 2200
ggcatttaac acccacctgg acttcagcag agtgggtccg ggccaaccag 2250
ccatgggacg gtcaccacg agtgccgggc tgggctctgc ggtgcggtcc 2300
acgggagagc aggcctccag ctggaaaggc caggcctgga gcttgcctct 2350
tcagtttttg tggcagtttt agttttttgt ttttttttt tttaatcaaa 2400
aaacaatttt ttttaaaaaa aagctttgaa aatggatggt ttgggtatta 2450
aaaagaaaaa aaaaacttaa aaaaaaaaag acactaacgg ccagtgaagt 2500
ggagtctcag ggcaggggtg cagtttccct tgagcaaagc agccagacgt 2550
tgaactgtgt ttcctttccc tgggcgcagg gtgcaggggt tcttccgat 2600
ctgggtgtgac cttgggtccag gagttctatt tgttcctggg gaggaggtt 2650
tttttgtttg ttttttgggt ttttttgggt tcttgttttc tttctcctcc 2700
atgtgtcttg gcaggcactc atttctgtgg ctgtcggcca gagggaatgt 2750
tctggagctg ccaaggaggg aggagactcg ggttggttaa tccccgatg 2800
aacggtgtc cattcgcacc tcccctcctc gtgcctgcc tgcctctcca 2850
cgcacagtgt taaggagcca agaggagcca cttcgcccag actttgtttc 2900
cccacctcct gcggcatggg tgtgtccagt gccaccgtg gcctccgtg 2950
cttccatcag cctgtcgcc acctggtcct tcatgaagag cagacactta 3000
gaggctgtc gggaaatgggg aggtcgcccc tgggagggca ggcgttggtt 3050
ccaagccggt tcccgctcct ggcgcctgga gtgcacacag cccagtcggc 3100
acctggtggc tggaagccaa cctgctttag atcactcggg tccccacctt 3150
agaaggggtc ccgccttaga tcaatcacgt ggacactaag gcacgtttta 3200
gagtctcttg tcttaatgat tatgtccatc cgtctgtccg tccatttgtg 3250
ttttctgcgt cgtgtcattg gatataatcc tcagaaataa tgcacactag 3300

cctctgacaa ccatgaagca aaaatccgtt acatgtgggt ctgaacttgt 3350
agactcgggtc acagtatcaa ataaaaatcta taacagaaaa aaaaaaaaaa 3400
a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1				5					10					15
Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
				20					25					30
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
				35					40					45
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
				50					55					60
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
				65					70					75
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
				80					85					90
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys
				95					100					105
Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro
				110					115					120
Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu
				125					130					135
Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp
				140					145					150
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu
				155					160					165
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp
				170					175					180
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val
				185					190					195
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu
				200					205					210
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala
				215					220					225

Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp
				230					235					240
Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu
				245					250					255
Glu	Leu	His	Leu	Thr	Gly	Asn	Leu	Ser	Ala	Glu	Asn	Asn	Arg	Tyr
				260					265					270
Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu
				275					280					285
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp
				290					295					300
Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr
				305					310					315
Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr
				320					325					330
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser
				335					340					345
Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Asn
				350					355					360
Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly

	500		505		510
Glu Cys Pro Leu	Leu Lys Arg Ser Gly	Leu Val Val Glu Glu	Asp		
	515		520		525
Leu Phe Asn Thr	Leu Pro Pro Glu Val	Lys Glu Arg Leu Trp	Arg		
	530		535		540
Ala Asp Lys Glu	Gln Ala				
	545				

<210> 251
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 251
 caacaatgag ggcaccaagc 20

<210> 252
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 252
 gatggctagg ttctggaggt tctg 24

<210> 253
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 253
 caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254
 <211> 1650
 <212> DNA
 <213> Homo Sapien

<400> 254
 gcctgttgct gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50
 gcgctctccc gtcccgcggg ggttgctgct gctgccgctg ctgctgggcc 100
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200

ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250
ggcttcaggg cgggtccaggc ggttctagca ctggatttgg aaactttgag 300
gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350
ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400
gttatgtgaa tggtagtggg gcctatgcca aggacctggc tatggtggct 450
tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500
ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550
cagctggcat tggcttagag ctttataagg ccattcagcg agggaccatc 600
aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctcccctgt 650
tgattcgggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700
aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750
gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800
agaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850
taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900
cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950
agatgcctta agccagctca tgaatggccc catcagaaag aagctcaaaa 1000
ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050
aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100
gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150
tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200
gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgacct 1250
taaattcttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300
tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350
atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400
gggctggaga tgagctgggt tggccttggg gcacagagct gagctgaggc 1450
cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500
gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550
ggaggcaatt tggaaattat ttctgcttct taaaaaacc taagattttt 1600

taaaaaattg atttgttttg atcaaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1				5					10					15

Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
				20					25					30

Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35					40					45

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn
				50					55					60

Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln
				65					70					75

Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu
				80					85					90

Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp
				95					100					105

Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr
				110					115					120

Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu
				125					130					135

Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe
				140					145					150

Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser
				155					160					165

Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu
				170					175					180

Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly
				185					190					195

Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu
				200					205					210

Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys
				215					220					225

Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala
				230					235					240

Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	245	250	255
Ala Glu Met Ile	Ile Glu Gln Asn Thr	Asp Gly Val Asn Phe	Tyr
	260	265	270
Asn Ile Leu Thr	Lys Ser Thr Pro Thr	Ser Thr Met Glu Ser	Ser
	275	280	285
Leu Glu Phe Thr	Gln Ser His Leu Val	Cys Leu Cys Gln Arg	His
	290	295	300
Val Arg His Leu	Gln Arg Asp Ala Leu	Ser Gln Leu Met Asn	Gly
	305	310	315
Pro Ile Arg Lys	Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser	Trp
	320	325	330
Gly Gly Gln Ala	Thr Asn Val Phe Val	Asn Met Glu Glu Asp	Phe
	335	340	345
Met Lys Pro Val	Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala	Gly
	350	355	360
Ile Asn Val Thr	Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val	Asp
	365	370	375
Thr Met Gly Gln	Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro	Glu
	380	385	390
Leu Pro Lys Phe	Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser	Asp
	395	400	405
Pro Lys Ser Leu	Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys	Asn
	410	415	420
Leu Ala Phe Tyr	Trp Ile Leu Lys Ala	Gly His Met Val Pro	Ser
	425	430	435
Asp Gln Gly Asp	Met Ala Leu Lys Met	Met Arg Leu Val Thr	Gln
	440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50

tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250
 ctcacggcgg cgactgctt tgaacacctat agtgacctta gtgatccctc 300
 cgggtgggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
 gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400
 cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450
 tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550
 tacatcaaag aggatgaggc actgccatct cccacacccc tccaggaagt 600
 tcaggtcgcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650
 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700
 caaggcggga aggatgcctg cttcggtgac tcagggtggac ccttggcctg 750
 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800
 gctgtggtcg gcccaatcgg ccggtgtct acaccaatat cagccaccac 850
 tttgagtgga tccagaagct gatggcccag agtggcatgt cccagccaga 900
 cccctcctgg ccactactct tttccctct tctctgggct ctcccactcc 950
 tggggccggt ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000
 agtcaggccc tggttctctt ctgtcttggt tggtaataaa cacattccag 1050
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
1				5					10					15
Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
				20					25					30
Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
			35						40					45
Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
			50						55					60
Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
			65						70					75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu	80	85	90
Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser	95	100	105
Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe	110	115	120
Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro	125	130	135
Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr	140	145	150
Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe	155	160	165
Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys	170	175	180
Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln	185	190	195
Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe	Leu	Lys	200	205	210
Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly	215	220	225
Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly	230	235	240
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	245	250	255
Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	260	265	270
Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met	275	280	285
Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu	290	295	300
Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val		305	310	

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

cctcctaggg ctctttgccc tcacccctctc tggcaaatgc agttacagcc 100
cggagcccga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150
cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200
gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250
ctcctcaata cggaaaatac ctgaccctag agaatgtggc tgatctgggtg 300
aggccatccc cactgaccct ccacacgggtg caaaaatggc tcttggcagc 350
cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400
ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450
cactatgtgg gaggacctac ggaaacccat gttgtaaggt cccacatcc 500
ctaccagctt ccacaggcct tggcccccca tgtggacttt gtggggggac 550
tgcaccgttt tcccccaaca tcacccctga ggcaacgtcc tgagccgcag 600
gtgacaggga ctgtaggcct gcacctgggg gtaacccct ctgtgatccg 650
taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700
acagccaagc ctgtgcccag ttcctggagc agtatttcca tgactcagac 750
ctggctcagt tcacgcgcct cttcgggtggc aactttgcac atcaggcatc 800
agtagcccggt gtggttgagc aacaggggccg gggccggggc gggattgagg 850
ccagtctaga tgtgcagtac ctgatgagtg ctggtgcca catctccacc 900
tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttcctgca 950
gtggctcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000
tgagctatgg agatgatgag gactccctca gcagcgccta catccagcgg 1050
gtcaacactg agctcatgaa ggctgccgct cggggtctca ccctgctctt 1100
cgcctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150
agttccgccc taccttccct gcctccagcc cctatgtcac cacagtggga 1200
ggcacatcct tccaggaacc tttcctcatc acaaatgaaa ttgttgacta 1250
tatcagtgggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300
aggaagctgt aacgaagttc ctgagctcta gccccacct gccaccatcc 1350
agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400
tgatggctac tgggtgtgca gcaacagagt gccattcca tgggtgtccg 1450
gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500

gagcacagga tccttagtgg ccgccccct cttggctttc tcaaccaag 1550
gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600
atgagtcctg tctggatgaa gaggtagagg gccagggttt ctgctctggt 1650
cctggctggg atcctgtaac aggctgggga acaccaactt cccagctttg 1700
ctgaagactc tactcaaccc ctgacccttt cctatcagga gagatggctt 1750
gtccccctgcc ctgaagctgg cagttcagtc ccttattctg ccctggtgga 1800
agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850
aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900
atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950
gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000
ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050
acttgatatt cattcccca ttcactgcaa ggagacctct actgtcaccg 2100
tttactcttt cctaccctga catccagaaa caatggcctc cagtgcatac 2150
ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200
ccttacttag cttccaggtc ttaacttctc tgactactct tgtcttcctc 2250
tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300
tgtagatttt tgctcttctc agtttactca ttgtcccctg gaacaaatca 2350
ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400
aatgattgat acctcaaatg taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1				5				10					15	
Ser	Gly	Lys	Cys	Ser	Tyr	Ser	Pro	Glu	Pro	Asp	Gln	Arg	Arg	Thr
				20				25					30	
Leu	Pro	Pro	Gly	Trp	Val	Ser	Leu	Gly	Arg	Ala	Asp	Pro	Glu	Glu
			35					40					45	
Glu	Leu	Ser	Leu	Thr	Phe	Ala	Leu	Arg	Gln	Gln	Asn	Val	Glu	Arg
			50					55					60	

Leu	Ser	Glu	Leu	Val	Gln	Ala	Val	Ser	Asp	Pro	Ser	Ser	Pro	Gln	
				65					70					75	
Tyr	Gly	Lys	Tyr	Leu	Thr	Leu	Glu	Asn	Val	Ala	Asp	Leu	Val	Arg	
				80					85					90	
Pro	Ser	Pro	Leu	Thr	Leu	His	Thr	Val	Gln	Lys	Trp	Leu	Leu	Ala	
				95					100					105	
Ala	Gly	Ala	Gln	Lys	Cys	His	Ser	Val	Ile	Thr	Gln	Asp	Phe	Leu	
				110					115					120	
Thr	Cys	Trp	Leu	Ser	Ile	Arg	Gln	Ala	Glu	Leu	Leu	Leu	Pro	Gly	
				125					130					135	
Ala	Glu	Phe	His	His	Tyr	Val	Gly	Gly	Pro	Thr	Glu	Thr	His	Val	
				140					145					150	
Val	Arg	Ser	Pro	His	Pro	Tyr	Gln	Leu	Pro	Gln	Ala	Leu	Ala	Pro	
				155					160					165	
His	Val	Asp	Phe	Val	Gly	Gly	Leu	His	Arg	Phe	Pro	Pro	Thr	Ser	
				170					175					180	
Ser	Leu	Arg	Gln	Arg	Pro	Glu	Pro	Gln	Val	Thr	Gly	Thr	Val	Gly	
				185					190					195	
Leu	His	Leu	Gly	Val	Thr	Pro	Ser	Val	Ile	Arg	Lys	Arg	Tyr	Asn	
				200					205					210	
Leu	Thr	Ser	Gln	Asp	Val	Gly	Ser	Gly	Thr	Ser	Asn	Asn	Ser	Gln	
				215					220					225	
Ala	Cys	Ala	Gln	Phe	Leu	Glu	Gln	Tyr	Phe	His	Asp	Ser	Asp	Leu	
				230					235					240	
Ala	Gln	Phe	Met	Arg	Leu	Phe	Gly	Gly	Asn	Phe	Ala	His	Gln	Ala	
				245					250					255	
Ser	Val	Ala	Arg	Val	Val	Gly	Gln	Gln	Gly	Arg	Gly	Arg	Ala	Gly	
				260					265					270	
Ile	Glu	Ala	Ser	Leu	Asp	Val	Gln	Tyr	Leu	Met	Ser	Ala	Gly	Ala	
				275					280					285	
Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	
				290					295					300	
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	
				305					310					315	
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	
				320					325					330	
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	
				335					340					345	

Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	350	355	360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	365	370	375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	380	385	390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	395	400	405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	410	415	420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	425	430	435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	440	445	450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	455	460	465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	470	475	480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	485	490	495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	500	505	510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	515	520	525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	530	535	540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	545	550	555

Cys

<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

<400> 260

gccgcgcgct ctctcccggc gccacacct gtctgagcgg cgcagcgagc 50

cgcggccccg gcgggctgct cggcgcggaa cagtgctcgg catggcaggg 100

attccagggc tcctcttctt tctcttcttt ctgctctgtg ctgttgggca 150

agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200

tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taagggaact ccactgcccc cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggagccgca cagagacgca ggtgggcatc 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttctgtctca actacccttt ctcaacatca 550
gtgaagtatt ccacgggctg caccggcacc ctgggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttctaaagc ccaagtttaa agatgggtgt 700
cgagggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caaggggttg atcaagggca 800
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcttgctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctggggt 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100
ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150
gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200
ctattggatt aaaggaaact acctggattg tagggagggg tgacacagt 1250
ttccctcctg gcagcaatta agggctctca tgttcttatt ttaggagagg 1300
ccaaattggt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350
tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400
tgactggctt tactatttga aaactgggtt gtgtatcata tcatatatca 1450
tttaagcagt ttgaaggcat acttttgcac agaaataaaa aaaatactga 1500
tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550
caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600

atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
1				5					10					15

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
			20						25					30

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
			35						40					45

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
				50					55					60

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
				65					70					75

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
			80						85					90

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
				95					100					105

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
				110					115					120

Ser	Gly	Lys	Ser	Arg	Arg	Lys	Arg	Gln	Ile	Tyr	Gly	Tyr	Asp	Ser
				125					130					135

Arg	Phe	Ser	Ile	Phe	Gly	Lys	Asp	Phe	Leu	Leu	Asn	Tyr	Pro	Phe
				140					145					150

Ser	Thr	Ser	Val	Lys	Leu	Ser	Thr	Gly	Cys	Thr	Gly	Thr	Leu	Val
				155					160					165

Ala	Glu	Lys	His	Val	Leu	Thr	Ala	Ala	His	Cys	Ile	His	Asp	Gly
				170					175					180

Lys	Thr	Tyr	Val	Lys	Gly	Thr	Gln	Lys	Leu	Arg	Val	Gly	Phe	Leu
				185					190					195

Lys	Pro	Lys	Phe	Lys	Asp	Gly	Gly	Arg	Gly	Ala	Asn	Asp	Ser	Thr
				200					205					210

Ser	Ala	Met	Pro	Glu	Gln	Met	Lys	Phe	Gln	Trp	Ile	Arg	Val	Lys
				215					220					225

Arg	Thr	His	Val	Pro	Lys	Gly	Trp	Ile	Lys	Gly	Asn	Ala	Asn	Asp
				230					235					240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu	Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys Phe Met Lys Ile Gly	Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly Gly Arg Ile His Phe	Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn Leu Val Tyr Arg Phe	Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys	Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly Val Tyr Val Arg Met	Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg Lys Ile Ile Gly Ile	Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn Gly Ser Pro Gln Asp	Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile	Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp Cys Arg Glu Gly		380		

<210> 262
 <211> 1378
 <212> DNA
 <213> Homo Sapien

<400> 262
 gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50
 ccatgggtggt ttctggagcg ccccagccc tgggtggggg ctgtctcggc 100
 accttcacct ccctgctgct gctggcgctcg acagccatcc tcaatgcggc 150
 caggatacct gttccccag cctgtgggaa gcccagcag ctgaaccggg 200
 ttgtgggagg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
 atccagaaga atgggaccca cactgcgca ggttctctgc tcaccagccg 300
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaacct 350
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
 cgggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450
 ctggaaggaa ggtgcctgtg cagacattgc cctgggtgct ctcgagcgct 500
 ccatacagtt ctgagagcg gtcctgcca tctgcctacc tgatgcctct 550

atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650
 ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700
 ggacaggggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850
 gccgagcgca acaggcccg ggtctacatc agcctctctg cgcaccgctc 900
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950
 ggggtggggc cctcaggga ccgagccagg gctctggggc cgccgcgcgc 1000
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050
 cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100
 aataggctca tctacctta cctctggggg cccggacggc tgctgcggaa 1150
 aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200
 catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250
 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300
 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
1				5					10					15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
				20					25					30
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35					40					45
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50					55					60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65					70					75

Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180
Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu	185	190	195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His	200	205	210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met	215	220	225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly	230	235	240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu	245	250	255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn	260	265	270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val	275	280	285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly	290	295	300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala	305	310	315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264
gtccgcaagg atgcctacat gttc 24

<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 265
gcagagggtg ctaagggtg 19

<210> 266
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
ggggaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269

gaatgccctg caagcatcaa ctgg 24

<210> 270

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 270

gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 271

gcggaagggc agaatgggac tccaag 26

<210> 272

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 272

cagccctgcc acatgtgc 18

<210> 273

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 273

tactgggtgg tcagcaac 18

<210> 274

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 274

ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
gggcagggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgatt gctggttagag caag 24

<210> 280

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 280
ttacagtgcc ccctggaaac ccacttg gcc tgcataccgc ctccc 45

<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gtcctataga gttcccttgc ccca 34

<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 282
tggaggggga gcgggatgct tgtctggg cg actccggggg cccctcatg 50
tgccaggtgg a 61

<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 283
ccctcagacc ctgcagaagc tgaagggtcc tatcatcgac tcggaagtct 50
gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100
atgctgtgtg ccggctact 119

<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien

<400> 284
gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100
agatgaggag aaacgtttga tgggtggagct gcacaacctc taccggggccc 150
aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt gggggccaaa 250
caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300
gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350
tacaacctca gcgcccgcac ctgcagccca ggccagatgt gcggccacta 400
cacgcaggtg gtatgggcca agacagagag gatcgggtgt ggttcccact 450
tctgtgagaa gctccagggg gttgaggaga ccaacatcga attactggtg 500
tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550
ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600
tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650
gtaactgagg ccccatcctt ccggggcgact gaagcatcag actctaggaa 700
aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750
cagaggtctc aggctccctg gcaaccaagg ctctgcctgc tgtggaaacc 800
caggccccaa cttccttagc aacgaaagac ccgccctcca tggcaacaga 850
ggctccacct tgcgtaacaa ctgaggtccc ttccattttg gcagctcaca 900
gcctgcctc cttggatgag gagccagtta ccttccccaa atcgacccat 950
gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000
ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050
caagggaact cctaccccat gcccaggagg aggctgaggc tgaggctgag 1100
ttgcctcctt ccagtgaggt cttggcctca gtttttccag ccaggacaa 1150
gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200
agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250
gggctgcccc tggctctgca gtcgtccttg ccaggtgcag agggccctga 1300
caagcctagc gttgtgtcag ggctgaactc gggccctggt catgtgtggg 1350
gccctctcct gggactactg ctctgcctc ctctggtgtt ggctggaatc 1400
ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450
catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500

ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600
 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700
 tgccacaca gcatgtgctc tctccctgag tgcctgtgta gctggggatg 1750
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800
 tgagtggggg aggcagggac gagggaagga aagtaactcc tgactctcca 1850
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu			
1				5					10					15			
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp			
				20					25					30			
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala			
				35					40					45			
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp			
				50					55					60			
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val			
				65					70					75			
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe			
				80					85					90			
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu			
				95					100					105			
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys			
				110					115					120			
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala			
				125					130					135			
Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu			
				140					145					150			
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr			
				155					160					165			
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly			

170										175					180				
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser					
				185					190					195					
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro					
				200					205					210					
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser					
				215					220					225					
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile					
				230					235					240					
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys					
				245					250					255					
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr					
				260					265					270					
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr					
				275					280					285					
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu					
				290					295					300					
Asp	Glu	Glu	Pro	Val	Thr	Phe	Pro	Lys	Ser	Thr	His	Val	Pro	Ile					
				305					310					315					
Pro	Lys	Ser	Ala	Asp	Lys	Val	Thr	Asp	Lys	Thr	Lys	Val	Pro	Ser					
				320					325					330					
Arg	Ser	Pro	Glu	Asn	Ser	Leu	Asp	Pro	Lys	Met	Ser	Leu	Thr	Gly					
				335					340					345					
Ala	Arg	Glu	Leu	Leu	Pro	His	Ala	Gln	Glu	Glu	Ala	Glu	Ala	Glu					
				350					355					360					
Ala	Glu	Leu	Pro	Pro	Ser	Ser	Glu	Val	Leu	Ala	Ser	Val	Phe	Pro					
				365					370					375					
Ala	Gln	Asp	Lys	Pro	Gly	Glu	Leu	Gln	Ala	Thr	Leu	Asp	His	Thr					
				380					385					390					
Gly	His	Thr	Ser	Ser	Lys	Ser	Leu	Pro	Asn	Phe	Pro	Asn	Thr	Ser					
				395					400					405					
Ala	Thr	Ala	Asn	Ala	Thr	Gly	Gly	Arg	Ala	Leu	Ala	Leu	Gln	Ser					
				410					415					420					
Ser	Leu	Pro	Gly	Ala	Glu	Gly	Pro	Asp	Lys	Pro	Ser	Val	Val	Ser					
				425					430					435					
Gly	Leu	Asn	Ser	Gly	Pro	Gly	His	Val	Trp	Gly	Pro	Leu	Leu	Gly					
				440					445					450					
Leu	Leu	Leu	Leu	Pro	Pro	Leu	Val	Leu	Ala	Gly	Ile	Phe							

<210> 286
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 286
tcctgcagtt tcctgatgc 19

<210> 287
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 287
ctcatattgc acaccagtaa ttcg 24

<210> 288
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 288
atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien

<400> 289
gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50
tcattctcca agttatgggtg gacgtacttc tgttgttctc cctctgcttg 100
ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150
caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200
acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250
attacacttc tctccttggc tggaacagg attgttgaaa tactccctga 300
acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350
atatttcaga gtcctcaaact gcatttccag ccctacagct caaatatctg 400

tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450
tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500
ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550
aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600
tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650
atggagcttt ttgggggctg agcaacatgg aaattttgca gctggaccat 700
aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750
gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800
cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850
ttatcaaggt tagatgattc aagcttcctt ggcctaagct tactaaatac 900
actgcacatt gggaacaaca gagtcagcta cattgctgat tgtgccttcc 950
gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000
tggactattg aagacatgaa tgggtgctttc tctgggcttg acaaactgag 1050
gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100
tcactggttt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150
atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200
gcatttaaata acatcaagcc ttttgtgcca ttgccagcta aaatggctcc 1250
cacagtgggt ggcggaatac aactttcaga gctttgtaaa tgccagttgt 1300
gccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350
tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400
aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450
gccagcagca gtgattcccc aatgactttt gcttggaaaa aagacaatga 1500
actactgcat gatgctgaaa tggaaaatta tgcacacctc cggggccaag 1550
gtggcgaggt gatggagtat accaccatcc ttcggctgcg cgaggtggaa 1600
tttgccagtg aggggaaata tcagtgtgtc atctccaatc actttggttc 1650
atcctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700
ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750
gagtgtgctg ctgtggggca cccagcccc cagatagcct ggcagaagga 1800
tgggggcaca gacttcccag ctgcacggga gagacgcatg catgtgatgc 1850

ccgaggatga cgtgttcttt atcgtggatg tgaagataga ggacattggg 1900
gtatacagct gcacagctca gaacagtgca ggaagtatth cagcaaagtc 1950
aactctgact gtcctagaaa caccatcatt ttgctggcca ctgttggaac 2000
gaactgtaac caagggagaa acagccgtcc tacagtgcac tgctggagga 2050
agccctcccc ctaaaactgaa ctggaccaa gatgatagcc cattgggtgg 2100
aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150
actcagatgt cagtgatgct gggaaataca catgtgagat gtctaacc 2200
cttggcactg agagaggaaa cgtgcgcctc agtgtgatcc ccactccaac 2250
ctgcgactcc cctcagatga cagccccatc gttagacgat gacggatggg 2300
ccactgtggg tgcctgatc atagccgtgg ttgctgtgt ggtgggcacg 2350
tcactcgtgt ggggtggcat catataccac acaaggcgga ggaatgaaga 2400
ttgcagcatt accaacacag atgagaccaa cttgccagca gatattccta 2450
gttatttgtc atctcaggga acgttagctg acaggcagga tgggtacgtg 2500
tcttcagaaa gtggaagcca ccaccagttt gtcacatctt caggtgctgg 2550
atttttctta ccacaacatg acagtagtgg gacctgccat attgacaata 2600
gcagtgaagc tgatgtggaa gctgccacag atctgttctt ttgtccgttt 2650
ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700
tccttttgaa acatatcata caggttgagc tcctgacca agaacagttt 2750
taatggacca ctatgagccc agttacataa agaaaaagga gtgctacca 2800
tgttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatatc 2850
gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900
aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950
agtgcaaatc cagagccagc gtcggttgcc tcgagtaatt ctttcatggg 3000
tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050
ttggacagcc atcagattgt cagccaagag ctttttattt gaaagctcat 3100
tcttccccag acttggaactc tgggtcagag gaagatggga aagaaaggac 3150
agattttcag gaagaaaatc acatttgtac ctttaaagag acttttagaaa 3200
actacaggac tccaaatttt cagtcttatg acttggaac atagactgaa 3250

tgagaccaa ggaaaagctt aacatactac ctcaagtga cttttattta 3300
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350
 ataaaaatgc tttatttata cagatgaacc aaaattacaa aaagttatga 3400
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaacta 3450
 ttttttaact ttgttttatg caaaaaagta tcttacgtaa attaatagata 3500
 taaatcatga ttattttatg tatttttata atgccagatt tctttttatg 3550
 gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650
 tgtcaatttg aa 3662

<210> 290
 <211> 1059
 <212> PRT
 <213> Homo Sapien

<400> 290
 Met Val Asp Val Leu Leu Leu Phe Ser Leu Cys Leu Leu Phe His
 1 5 10 15
 Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
 20 25 30
 Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
 35 40 45
 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
 50 55 60
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
 65 70 75
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
 80 85 90
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
 95 100 105
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
 110 115 120
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
 125 130 135
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
 140 145 150
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
 155 160 165

Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	290	295	300
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile	305	310	315
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg	320	325	330
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala	335	340	345
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn	350	355	360
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys	365	370	375
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys	380	385	390
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln	395	400	405
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly	410	415	420
Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp	425	430	435
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala	440	445	450

Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser	455	460	465
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu	470	475	480
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln	485	490	495
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu	500	505	510
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn	515	520	525
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn	530	535	540
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg	545	550	555
Ala	Gly	Ala	Met	Ala	Arg	Leu	Glu	Cys	Ala	Ala	Val	Gly	His	Pro	560	565	570
Ala	Pro	Gln	Ile	Ala	Trp	Gln	Lys	Asp	Gly	Gly	Thr	Asp	Phe	Pro	575	580	585
Ala	Ala	Arg	Glu	Arg	Arg	Met	His	Val	Met	Pro	Glu	Asp	Asp	Val	590	595	600
Phe	Phe	Ile	Val	Asp	Val	Lys	Ile	Glu	Asp	Ile	Gly	Val	Tyr	Ser	605	610	615
Cys	Thr	Ala	Gln	Asn	Ser	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ala	Thr	620	625	630
Leu	Thr	Val	Leu	Glu	Thr	Pro	Ser	Phe	Leu	Arg	Pro	Leu	Leu	Asp	635	640	645
Arg	Thr	Val	Thr	Lys	Gly	Glu	Thr	Ala	Val	Leu	Gln	Cys	Ile	Ala	650	655	660
Gly	Gly	Ser	Pro	Pro	Pro	Lys	Leu	Asn	Trp	Thr	Lys	Asp	Asp	Ser	665	670	675
Pro	Leu	Val	Val	Thr	Glu	Arg	His	Phe	Phe	Ala	Ala	Gly	Asn	Gln	680	685	690
Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	695	700	705
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val	710	715	720
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met			

				725					730					735
Thr	Ala	Pro	Ser	Leu 740	Asp	Asp	Asp	Gly	Trp 745	Ala	Thr	Val	Gly	Val 750
Val	Ile	Ile	Ala	Val 755	Val	Cys	Cys	Val	Val 760	Gly	Thr	Ser	Leu	Val 765
Trp	Val	Val	Ile	Ile 770	Tyr	His	Thr	Arg	Arg 775	Arg	Asn	Glu	Asp	Cys 780
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro
				785					790					795
Ser	Tyr	Leu	Ser	Ser 800	Gln	Gly	Thr	Leu	Ala 805	Asp	Arg	Gln	Asp	Gly 810
Tyr	Val	Ser	Ser	Glu 815	Ser	Gly	Ser	His	His 820	Gln	Phe	Val	Thr	Ser 825
Ser	Gly	Ala	Gly	Phe 830	Phe	Leu	Pro	Gln	His 835	Asp	Ser	Ser	Gly	Thr 840
Cys	His	Ile	Asp	Asn 845	Ser	Ser	Glu	Ala	Asp 850	Val	Glu	Ala	Ala	Thr 855
Asp	Leu	Phe	Leu	Cys 860	Pro	Phe	Leu	Gly	Ser 865	Thr	Gly	Pro	Met	Tyr 870
Leu	Lys	Gly	Asn	Val 875	Tyr	Gly	Ser	Asp	Pro 880	Phe	Glu	Thr	Tyr	His 885
Thr	Gly	Cys	Ser	Pro 890	Asp	Pro	Arg	Thr	Val 895	Leu	Met	Asp	His	Tyr 900
Glu	Pro	Ser	Tyr	Ile 905	Lys	Lys	Lys	Glu	Cys 910	Tyr	Pro	Cys	Ser	His 915
Pro	Ser	Glu	Glu	Ser 920	Cys	Glu	Arg	Ser	Phe 925	Ser	Asn	Ile	Ser	Trp 930
Pro	Ser	His	Val	Arg 935	Lys	Leu	Leu	Asn	Thr 940	Ser	Tyr	Ser	His	Asn 945
Glu	Gly	Pro	Gly	Met 950	Lys	Asn	Leu	Cys	Leu 955	Asn	Lys	Ser	Ser	Leu 960
Asp	Phe	Ser	Ala	Asn 965	Pro	Glu	Pro	Ala	Ser 970	Val	Ala	Ser	Ser	Asn 975
Ser	Phe	Met	Gly	Thr 980	Phe	Gly	Lys	Ala	Leu 985	Arg	Arg	Pro	His	Leu 990
Asp	Ala	Tyr	Ser	Ser 995	Phe	Gly	Gln	Pro	Ser 1000	Asp	Cys	Gln	Pro	Arg 1005

Ala	Phe	Tyr	Leu	Lys	Ala	His	Ser	Ser	Pro	Asp	Leu	Asp	Ser	Gly
				1010					1015					1020
Ser	Glu	Glu	Asp	Gly	Lys	Glu	Arg	Thr	Asp	Phe	Gln	Glu	Glu	Asn
				1025					1030					1035
His	Ile	Cys	Thr	Phe	Lys	Gln	Thr	Leu	Glu	Asn	Tyr	Arg	Thr	Pro
				1040					1045					1050
Asn	Phe	Gln	Ser	Tyr	Asp	Leu	Asp	Thr						
				1055										

<210> 291
 <211> 2906
 <212> DNA
 <213> Homo Sapien

<400> 291
 ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50
 ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100
 tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150
 gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
 acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
 ttggtgtgtt ctgacataaa taaataatct taaagcagct gttccctcc 300
 ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350
 agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
 gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450
 ggtgtggtgg tgttttcctt tctttttgaa tttcccacia gaggagagga 500
 aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550
 gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600
 tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650
 ttcatacaacc tccttttttt taaattttta ttccttttgg tatcaagatc 700
 atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750
 gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800
 ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850
 ataggtccta ggtttaacag ggccctatct gacccctgc ttgtggtgct 900
 gctggctctt caacttcttg tgggtggtgg tctggtgcgg gctcagacct 950
 gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtgtt 1000

cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050
gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100
agcacttgag gcacttgga atcctacagt tgagtaggaa ccatatcaga 1150
accattgaaa ttggggcttt caatgggtctg gcgaacctca acactctgga 1200
actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250
tgtctaaact gaaggagctc tgggttgcga acaaccccat tgaaagcatc 1300
ccttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350
ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggctctgt 1400
ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450
aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500
tttatctgcc atcaggcctg gctctttcca gggtttgatg caccttcaaa 1550
aactgtggat gatacagtc cagattcaag tgattgaacg gaatgccttt 1600
gacaaccttc agtcactagt ggagatcaac ctggcacaca ataactaac 1650
attactgcct catgacctct tcactccctt gcatcatcta gagcggatac 1700
atttacaatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750
tggtggataa aagacatggc cccctcgaac acagcttggt gtgcccgggtg 1800
taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850
attacttcac atgctatgct ccggtgattg tggagcccc tgcagacctc 1900
aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950
cctgacatct gtatcttggg ttactccaaa tggaacagtc atgacacatg 2000
gggcgtacaa agtgccgata gctgtgctca gtgatggtac gttaaatttc 2050
acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100
ttccgttggg aatactactg cttcagccac cctgaatggt actgcagcaa 2150
ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200
ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccactcc 2250
agtggctgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300
gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350
agtgggatcc caggaattga tgaggatcat aagactacca aaatcatcat 2400

tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450
 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500
 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550
 catggaaagc cacctgccc tgcctgctat cgagcatgag cacctaaatc 2600
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650
 ataaattcaa tacacagttc agtgcataaa ccgttattga tccgaatgaa 2700
 ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750
 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaacia 2850
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900
 caaaaa 2906

<210> 292
 <211> 640
 <212> PRT
 <213> Homo Sapien

<400> 292
 Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly
 1 5 10 15
 Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu
 20 25 30
 Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
 35 40 45
 Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
 50 55 60
 Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
 65 70 75
 Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
 80 85 90
 Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
 95 100 105
 Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
 110 115 120
 Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
 125 130 135
 Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
 140 145 150

Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser	155	160	165
Tyr	Ala	Phe	Asn	Arg	Ile	Pro	Ser	Leu	Arg	Arg	Leu	Asp	Leu	Gly	170	175	180
Glu	Leu	Lys	Arg	Leu	Ser	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	Glu	Gly	185	190	195
Leu	Ser	Asn	Leu	Arg	Tyr	Leu	Asn	Leu	Ala	Met	Cys	Asn	Leu	Arg	200	205	210
Glu	Ile	Pro	Asn	Leu	Thr	Pro	Leu	Ile	Lys	Leu	Asp	Glu	Leu	Asp	215	220	225
Leu	Ser	Gly	Asn	His	Leu	Ser	Ala	Ile	Arg	Pro	Gly	Ser	Phe	Gln	230	235	240
Gly	Leu	Met	His	Leu	Gln	Lys	Leu	Trp	Met	Ile	Gln	Ser	Gln	Ile	245	250	255
Gln	Val	Ile	Glu	Arg	Asn	Ala	Phe	Asp	Asn	Leu	Gln	Ser	Leu	Val	260	265	270
Glu	Ile	Asn	Leu	Ala	His	Asn	Asn	Leu	Thr	Leu	Leu	Pro	His	Asp	275	280	285
Leu	Phe	Thr	Pro	Leu	His	His	Leu	Glu	Arg	Ile	His	Leu	His	His	290	295	300
Asn	Pro	Trp	Asn	Cys	Asn	Cys	Asp	Ile	Leu	Trp	Leu	Ser	Trp	Trp	305	310	315
Ile	Lys	Asp	Met	Ala	Pro	Ser	Asn	Thr	Ala	Cys	Cys	Ala	Arg	Cys	320	325	330
Asn	Thr	Pro	Pro	Asn	Leu	Lys	Gly	Arg	Tyr	Ile	Gly	Glu	Leu	Asp	335	340	345
Gln	Asn	Tyr	Phe	Thr	Cys	Tyr	Ala	Pro	Val	Ile	Val	Glu	Pro	Pro	350	355	360
Ala	Asp	Leu	Asn	Val	Thr	Glu	Gly	Met	Ala	Ala	Glu	Leu	Lys	Cys	365	370	375
Arg	Ala	Ser	Thr	Ser	Leu	Thr	Ser	Val	Ser	Trp	Ile	Thr	Pro	Asn	380	385	390
Gly	Thr	Val	Met	Thr	His	Gly	Ala	Tyr	Lys	Val	Arg	Ile	Ala	Val	395	400	405
Leu	Ser	Asp	Gly	Thr	Leu	Asn	Phe	Thr	Asn	Val	Thr	Val	Gln	Asp	410	415	420
Thr	Gly	Met	Tyr	Thr	Cys	Met	Val	Ser	Asn	Ser	Val	Gly	Asn	Thr	425	430	435

Thr	Ala	Ser	Ala	Thr	Leu	Asn	Val	Thr	Ala	Ala	Thr	Thr	Thr	Pro
				440					445					450
Phe	Ser	Tyr	Phe	Ser	Thr	Val	Thr	Val	Glu	Thr	Met	Glu	Pro	Ser
				455					460					465
Gln	Asp	Glu	Ala	Arg	Thr	Thr	Asp	Asn	Asn	Val	Gly	Pro	Thr	Pro
				470					475					480
Val	Val	Asp	Trp	Glu	Thr	Thr	Asn	Val	Thr	Thr	Ser	Leu	Thr	Pro
				485					490					495
Gln	Ser	Thr	Arg	Ser	Thr	Glu	Lys	Thr	Phe	Thr	Ile	Pro	Val	Thr
				500					505					510
Asp	Ile	Asn	Ser	Gly	Ile	Pro	Gly	Ile	Asp	Glu	Val	Met	Lys	Thr
				515					520					525
Thr	Lys	Ile	Ile	Ile	Gly	Cys	Phe	Val	Ala	Ile	Thr	Leu	Met	Ala
				530					535					540
Ala	Val	Met	Leu	Val	Ile	Phe	Tyr	Lys	Met	Arg	Lys	Gln	His	His
				545					550					555
Arg	Gln	Asn	His	His	Ala	Pro	Thr	Arg	Thr	Val	Glu	Ile	Ile	Asn
				560					565					570
Val	Asp	Asp	Glu	Ile	Thr	Gly	Asp	Thr	Pro	Met	Glu	Ser	His	Leu
				575					580					585
Pro	Met	Pro	Ala	Ile	Glu	His	Glu	His	Leu	Asn	His	Tyr	Asn	Ser
				590					595					600
Tyr	Lys	Ser	Pro	Phe	Asn	His	Thr	Thr	Thr	Val	Asn	Thr	Ile	Asn
				605					610					615
Ser	Ile	His	Ser	Ser	Val	His	Glu	Pro	Leu	Leu	Ile	Arg	Met	Asn
				620					625					630
Ser	Lys	Asp	Asn	Val	Gln	Glu	Thr	Gln	Ile					
				635					640					

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

agccgacgct gctcaagctg caactctggt gcagttggca gttcttttcg 50

gtttccctcc tgctgtttgg gggcatgaaa gggcttcgcc gccgggagta 100

aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150

gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200

gcgcgcgctg ggagcttcgg gtagagacct aggccgctgg accgcgatga 250
gcgcgccgag cctccgtgcg cgcgccgcgg ggttggggct gctgctgtgc 300
gcggtgctgg ggcgcgctgg ccggtccgac agcggcggtc gcggggaact 350
cgggcagccc tctggggtag ccgccgagcg cccatgcccc actacctgcc 400
gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450
cccgagccac tcccgtcctg ggtcgcctcg ctggacttaa gtcacaacag 500
attatctttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550
aagtgaaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600
gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650
aatactccct gaacatctga aagagtttca gtcccttgaa actttggacc 700
ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750
ctcaaatact tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800
gtattttgac aatttggcca acacactcct tgtgttaaag ctgaacagga 850
accgaatctc agctatccca cccaagatgt ttaaactgcc ccaactgcaa 900
catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950
ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000
cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050
cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100
cttgctgatg ctgcaggaac ttcactctcag ccaaaatgcc atcaacagga 1150
tcagccctga tgccctggag ttctgccaga agctcagtga gctggacctt 1200
actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250
cttactaaat aactgcaca ttgggaacaa cagagtcagc tacattgctg 1300
attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350
aatgaaattt cctggactat tgaagacatg aatggtgctt tctctgggct 1400
tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450
ctaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500
gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aatgaagaa 1550
actgcaacaa ttgcatttaa atacatcaag ccttttgtgc gattgccagc 1600

taaaatggct cccacagtgg gtggcggaaa acaactttca gagctttgta 1650
aatgccagtt gtgcccattc tcagctgcta aaaggaagaa gcatttttgc 1700
tgtagccca gatggctttg tgtgtgatga ttttccaaa cccagatca 1750
cggttcagcc agaaacacag tcggcaataa aaggttcaa tttgagtttc 1800
atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttgga 1850
aaaagacaat gaactactgc atgatgctga aatggaaaat tatgcacacc 1900
tccgggcca aggtggcgag gtgatggagt ataccacat cttcggctg 1950
cgcgaggtgg aatttgccag tgaggggaaa tatcagtgtg tcatctcaa 2000
tcactttggt tcactctact ctgtcaaagc caagcttaca gtaaatatgc 2050
ttccctcatt caccaagacc cccatggatc tcaccatccg agctggggcc 2100
atggcacgct tggagtgtgc tgctgtgggg caccagccc cccagatagc 2150
ctggcagaag gatgggggca cagacttccc agctgcacgg gagagacgca 2200
tgcatgtgat gcccaggat gacgtgttct ttatcgtgga tgtgaagata 2250
gaggacattg gggatacag ctgcacagct cagaacagtg caggaagtat 2300
ttcagcaaat gcaactctga ctgtcctaga aacaccatca tttttgcggc 2350
cactgttga ccgaactgta accaaggag aaacagccgt cctacagtgc 2400
attgctggag gaagccctcc ccctaaactg aactggacca aagatgatag 2450
cccattggtg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500
tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550
atgtctaaca cccttggcac tgagagagga aacgtgcgcc tcagtgtgat 2600
ccccactcca acctgcgact ccctcagat gacagcccca tcgttagacg 2650
atgacggatg ggccactgtg ggtgtcgtga tcatagccgt ggtttgctgt 2700
gtggtgggca cgtcactcgt gtgggtggtc atcatatacc acacaaggcg 2750
gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800
cagatattcc tagttatttg tcatctcagg gaacgttagc tgacaggcag 2850
gatgggtacg tgtcttcaga aagtggaagc caccaccagt ttgtcacatc 2900
ttcaggtgct ggatttttct taccacaaca tgacagtagt gggacctgcc 2950
atattgacaa tagcagtga gctgatgtgg aagctgccac agatctgttc 3000
ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050

gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100
 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150
 gagtgctacc catgtttctca tccttcagaa gaatcctgcg aacggagctt 3200
 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250
 actctcacia tgaaggacct ggaatgaaaa atctgtgtct aaacaagtcc 3300
 tcttttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350
 ttctttcatg ggtacctttg gaaaagctct caggagacct cacctagatg 3400
 cctattcaag ctttggacag ccatcagatt gtcagccaag agccttttat 3450
 ttgaaagctc attcttcccc agacttggac tctgggtcag aggaagatgg 3500
 gaaagaaagg acagattttc aggaagaaaa tcacatttgt acctttaaac 3550
 agactttaga aaactacagg actccaaatt ttcagtctta tgacttggac 3600
 acatagactg aatgagacca aaggaaaagc ttaacatact acctcaagtg 3650
 aacttttatt taaaagagag agaatcttat gtttttttaa tggagttatg 3700
 aattttaaaa ggataaaaat gctttattta tacagatgaa ccaaaattac 3750
 aaaaagttat gaaaattttt ataactgggaa tgatgctcat ataagaatac 3800
 ctttttaaac tattttttta ctttgtttta tgcaaaaaag tatcttacgt 3850
 aaattaatga tataaatcat gattatttta tgtattttta taatgccaga 3900
 tttcttttta tggaaaatga gttactaaag catttttaaat aatacctgcc 3950
 ttgtaccatt ttttaaatag aagttacttc attatatattt gcacattata 4000
 ttttaataaaa tgtgtcaatt tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4050
 aaa 4053

<210> 294
 <211> 1119
 <212> PRT
 <213> Homo Sapien

<400> 294
 Met Ser Ala Pro Ser Leu Arg Ala Arg Ala Gly Leu Gly Leu
 1 5 10 15
 Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly
 20 25 30
 Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
 35 40 45

Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys	50	55	60
Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp	65	70	75
Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys	80	85	90
Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	95	100	105
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	110	115	120
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	125	130	135
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	140	145	150
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	155	160	165
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	170	175	180
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	185	190	195
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	200	205	210
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	215	220	225
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	230	235	240
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	245	250	255
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	260	265	270
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	275	280	285
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	290	295	300
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	305	310	315
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	320	325	330

Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	
				335					340					345	
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	
				350					355					360	
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile	
				365					370					375	
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg	
				380					385					390	
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala	
				395					400					405	
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn	
				410					415					420	
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys	
				425					430					435	
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys	
				440					445					450	
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln	
				455					460					465	
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly	
				470					475					480	
Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp	
				485					490					495	
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala	
				500					505					510	
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser	
				515					520					525	
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu	
				530					535					540	
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln	
				545					550					555	
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu	
				560					565					570	
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn	
				575					580					585	
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn	
				590					595					600	
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg	
				605					610					615	

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
620	625		630
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
635	640		645
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
650	655		660
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
665	670		675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
680	685		690
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
695	700		705
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
710	715		720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
725	730		735
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
740	745		750
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
755	760		765
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
770	775		780
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
785	790		795
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
800	805		810
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
815	820		825
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
830	835		840
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
845	850		855
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
860	865		870
Tyr Val Ser Ser	Glu Ser Gly Ser His	His Gln Phe Val Thr	Ser
875	880		885
Ser Gly Ala Gly	Phe Phe Leu Pro Gln	His Asp Ser Ser Gly	Thr
890	895		900

Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	905	910	915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	920	925	930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	935	940	945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	950	955	960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	965	970	975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	980	985	990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	995	1000	1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu	1010	1015	1020
Asp	Phe	Ser	Ala	Asn	Pro	Glu	Pro	Ala	Ser	Val	Ala	Ser	Ser	Asn	1025	1030	1035
Ser	Phe	Met	Gly	Thr	Phe	Gly	Lys	Ala	Leu	Arg	Arg	Pro	His	Leu	1040	1045	1050
Asp	Ala	Tyr	Ser	Ser	Phe	Gly	Gln	Pro	Ser	Asp	Cys	Gln	Pro	Arg	1055	1060	1065
Ala	Phe	Tyr	Leu	Lys	Ala	His	Ser	Ser	Pro	Asp	Leu	Asp	Ser	Gly	1070	1075	1080
Ser	Glu	Glu	Asp	Gly	Lys	Glu	Arg	Thr	Asp	Phe	Gln	Glu	Glu	Asn	1085	1090	1095
His	Ile	Cys	Thr	Phe	Lys	Gln	Thr	Leu	Glu	Asn	Tyr	Arg	Thr	Pro	1100	1105	1110
Asn	Phe	Gln	Ser	Tyr	Asp	Leu	Asp	Thr							1115		

<210> 295

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 295

ggaaccgaat ctcagcta 18

<210> 296
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 296
cctaaactga actggacca 19

<210> 297
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 297
ggctggagac actgaacct 19

<210> 298
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 298
acagctgcac agctcagaac agtg 24

<210> 299

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 299
cattcccagt ataaaaattt tc 22

<210> 300
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 300
gggtcttggt gaatgagg 18

<210> 301

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 301
gtgcctctcg gttaccacca atgg 24

<210> 302
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 302
gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 303
gcctttgaca accttcagtc actagtgg 28

<210> 304
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 304
cccatgtgt ccatgactgt tccc 24

<210> 305
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 305
tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 306
actccaagga aatcggatcc gttc 24

<210> 307
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
ttagcagctg aggatgggca caac 24

<210> 308
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 308
actccaagga aatcggatcc gttc 24

<210> 309
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 309
gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310
<211> 3296
<212> DNA
<213> Homo Sapien

<400> 310

caaaacttgc gtcgcgaggaga gcgcccagct tgacttgaat ggaaggagcc 50

cgagcccgcg gagcgagct gagactgggg gagcgcggttc ggcctgtggg 100

gcgccgctcg gcgccggggc gcagcagga aggggaagct gtggtctgcc 150

ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200

ccgtccccta tccctccttt atatagaaac cttccacact gggaaggcag 250
cggcgaggca ggagggctca tggtagagcaa ggaggccggc tgatctgcag 300
gcgcacagca ttccgagttt acagattttt acagatacca aatggaaggc 350
gaggaggcag aacagcctgc ctggttccat cagccctggc gcccaggcgc 400
atctgactcg gcaccccctg caggcaccat ggcccagagc cgggtgctgc 450
tgctcctgct gctgctgccg ccacagctgc acctgggacc tgtgcttgcc 500
gtgagggccc caggatttgg ccgaagtggc ggccacagcc tgagccccga 550
agagaacgaa tttgcggagg aggagccggt gctggtactg agccctgagg 600
agcccgggcc tggcccagcc gcggtcagct gccccgaga ctgtgcctgt 650
tcccaggagg gcgtcgtgga ctgtggcggc attgacctgc gtgagttccc 700
gggggacctg cctgagcaca ccaaccacct atctctgcag aacaaccagc 750
tggaaaagat ctaccctgag gagctctccc ggctgcaccg gctggagaca 800
ctgaacctgc aaaacaaccg cctgacttcc cgagggctcc cagagaaggc 850
gtttgagcat ctgaccaacc tcaattacct gtacttggcc aataacaagc 900
tgaccttggc accccgcttc ctgccaaacg ccctgatcag tgtggacttt 950
gctgccaaact atctcaccaa gatctatggg ctcacctttg gccagaagcc 1000
aaacttgagg tctgtgtacc tgcacaacaa caagctggca gacgccgggc 1050
tgccggacaa catgttcaac ggctccagca acgtcgaggt cctcatcctg 1100
tccagcaact tcctgcgcca cgtgcccag cacctgccgc ctgccctgta 1150
caagctgcac ctcaagaaca acaagctgga gaagatcccc ccgggggcct 1200
tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250
actgacgagg gcctggacaa cgagaccttc tggaagctct ccagcctgga 1300
gtacctggat ctgtccagca acaacctgtc tcgggtccca gctgggctgc 1350
cgcgcagcct ggtgctgctg cacttgagga agaacgcat ccggagcgtg 1400
gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450
cagcaaccag ctgcgggagc agggcatcca cccactggcc ttccagggcc 1500
tcaagcgggt gcacacggtg cacctgtaca acaacgcgt ggagcgcgtg 1550
cccagtggcc tgctcgcgcg cgtgcgcacc ctcgatgcc tgcacaacca 1600
gatcacaggc attggccgcg aagactttgc caccacctac ttcctggagg 1650

agctcaacct cagctacaac cgcataacca gcccacaggt gcaccgcgac 1700
gccttccgca agctgcgcct gctgcgctcg ctggacctgt cgggcaaccg 1750
gctgcacacg ctgccacctg ggctgcctcg aaatgtccat gtgctgaagg 1800
tcaagcgcaa tgagctggct gccttggcac gaggggctcg ggcgggcatg 1850
gctcagctgc gtgagctgta cctcaccagc aaccgactgc gcagccgagc 1900
cctgggcccc cgtgcctggg tggacctcgc ccatctgcag ctgctggaca 1950
tcgccgggaa tcagctcaca gagatccccg aggggctccc cgagtcactt 2000
gagtacctgt acctgcagaa caacaagatt agtgcggtgc ccgccaatgc 2050
cttcgactcc acgccaacc tcaaggggat ctttctcagg tttaacaagc 2100
tggctgtggg ctccgtgggtg gacagtgcct tccggaggct gaagcacctg 2150
caggtcttgg acattgaagg caacttagag tttggtgaca tttccaagga 2200
ccgtggccgc ttggggaagg aaaaggagga ggaggaagag gaggaggagg 2250
aggaagagga aacaagatag tgacaagggtg atgcagatgt gacctaggat 2300
gatggaccgc cggactcttt tctgcagcac acgcctgtgt gctgtgagcc 2350
ccccactctg ccgtgctcac acagacacac ccagctgcac acatgaggca 2400
tcccacatga cacgggctga cacagtctca tatccccacc ctttcccacg 2450
gcgtgtccca cggccagaca catgcacaca catcacaccc tcaaacaccc 2500
agctcagcca cacacaacta ccctccaaac caccacagtc tctgtcacac 2550
ccccactacc gctgccacgc cctctgaatc atgcagggaa gggctctgcc 2600
ctgccctggc acacacaggc acccattccc tccccctgct gacatgtgta 2650
tgcgtatgca tacacaccac acacacacac atgcacaagt catgtgcgaa 2700
cagccctcca aagcctatgc cacagacagc tcttgcccca gccagaatca 2750
gccatagcag ctgcgcgtct gccctgtcca tctgtccgtc cgttccctgg 2800
agaagacaca agggatatcca tgctctgtgg ccaggtgcct gccaccctct 2850
ggaactcaca aaagctggct ttatttcctt tccatccta tggggacagg 2900
agccttcagg actgctggcc tggcctggcc caccctgctc ctccagggtc 2950
tgggcagtca ctctgctaag agtccctccc tgccacgccc tggcaggaca 3000
caggcacttt tccaatgggc aagcccagtg gaggcaggat gggagagccc 3050

cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100
ctgggctgag ccagggagga aggaccagc tgcacctagg agacaccttt 3150
gttcttcagg cctgtggggg aagttccggg tgcctttatt tttattctt 3200
ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250
gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 311
gcattggccg cgagactttg cc 22

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 312
gcggccacgg tccttggaat tg 22

<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 313
tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien

<400> 314
gggagggggc tccggggcgc ggcagcagc cctgctccgg ccgcgcgct 50
cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggctgg 100
gggttcctcg agactctcag aggggcgcct cccatcggcg cccaccacc 150
caacctgttc ctgcgcgcc actgcgctgc gcccaggac ccgctgcca 200

acatggattt tctcctggcg ctggtgctgg tatcctcgct ctacctgcag 250
gcggccgccc agttcgacgg gaggtggccc aggcaaatag tgtcatcgat 300
tggcctatgt cgttatgggt ggaggattga ctgctgctgg ggctgggctc 350
gccagtcttg gggacagtgt cagcctgtgt gccaaaccacg atgcaaacat 400
ggtgaatgta tcggggccaaa caagtgaag tgtcatcctg gttatgctgg 450
aaaaacctgt aatcaagatc taaatgagtg tggcctgaag ccccgccct 500
gtaagcacag gtgcatgaac acttacggca gctacaagtg ctactgtctc 550
aacggatata tgctcatgcc ggatgggttc tgctcaagtg ccctgacctg 600
ctccatggca aactgtcagt atggctgtga tgttgtaaa ggacaaatac 650
ggtgccagtg cccatcccct ggctgcacc tggctcctga tgggaggacc 700
tgtgtagatg ttgatgaatg tgctacagga agagcctcct gccctagatt 750
taggcaatgt gtcaacactt ttgggagcta catctgcaag tgtcataaag 800
gcttcgatct catgtatatt ggaggcaaata atcaatgtca tgacatagac 850
gaatgctcac ttggtcagta tcagtgcagc agctttgctc gatgttataa 900
cgtacgtggg tcctacaagt gcaaagttaa agaaggatac cagggtgatg 950
gactgacttg tgtgtatatc ccaaaagtta tgattgaacc ttcagggtcca 1000
attcatgtac caaagggaaa tgggtaccatt ttaaagggtg acacaggaaa 1050
taataattgg attcctgatg ttggaagtac ttgggtggcct ccgaagacac 1100
catatattcc tcctatcatt accaacaggc ctacttctaa gccaacaaca 1150
agacctacac caaagccaac accaatcct actccaccac caccaccacc 1200
cctgccaaca gagctcagaa cacctctacc acctacaacc ccagaaaggc 1250
caaccaccgg actgacaact atagcaccag ctgccagtac acctccagga 1300
gggattacag ttgacaacag ggtacagaca gaccctcaga aaccagagg 1350
agatgtgttc agtgttctgg tacacagttg taattttgac catggacttt 1400
gtggatggat caggggagaaa gacaatgact tgcactggga accaatcagg 1450
gaccagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500
gggaaaagct gcacgcttgg tgctacctct cggccgcctc atgcattcag 1550
gggacctgtg cctgtcattc aggcacaagg tgacggggct gcactctggc 1600
acactccagg tgtttgtgag aaaacacggt gccacggag cagccctgtg 1650

gggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700
gggctgacat caagagcgaa tcacaaagat gattaaaggg ttggaaaaaa 1750
agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800
agaagactga ggggcaaacc attgatgggtt ttcaagtata tgaagggttg 1850
gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900
caagaggaaa ctggcttaga ctagagtata agggagcatt tcttggcagg 1950
ggccattgtt agaatacttc ataaaaaag aagtgtgaaa atctcagtat 2000
ctctctctct ttctaaaaaa ttagataaaa atttgtctat ttaagatggt 2050
taaagatgtt cttaccaag gaaaagtaac aaattataga atttcccaa 2100
agatgttttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150
taatttggac aaggcttaat ttaggcattt ccctcttgac ctctaatgg 2200
agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250
tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300
tattccaaat gagagtatga tggacagata ttttagtatc tcagtaatgt 2350
cctagtgtgg cggtggtttt caatgtttct tcatggtaaa ggtataagcc 2400
tttcatttgt tcaatggatg atgtttcaga tttttttttt tttaagagat 2450
ccttcaagga acacagttca gagagatttt catcgggtgc attctctctg 2500
cttcgtgtgt gacaagttat cttggctgct gagaaagagt gccctgcccc 2550
acaccggcag acctttcctt cacctcatca gtatgattca gtttctctta 2600
tcaattggac tctcccagg tccacagaac agtaatat tttgaacaat 2650
aggtacaata gaaggtcttc tgtcatttaa cctggtaaag gcagggctgg 2700
agggggaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750
gtagatccat ttttaatggt tcatttcctt tatggtcata taactgcaca 2800
gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850
tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900
catcttgttt attatttaat gttttctaaa ataaaaaatg ttagtgggtt 2950
tccaaatggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000
aat 3003

<210> 315
 <211> 509
 <212> PRT
 <213> Homo Sapien

<400> 315

Met	Asp	Phe	Leu	Leu	Ala	Leu	Val	Leu	Val	Ser	Ser	Leu	Tyr	Leu	1	5	10	15
Gln	Ala	Ala	Ala	Glu	Phe	Asp	Gly	Arg	Trp	Pro	Arg	Gln	Ile	Val	20	25	30	
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	35	40	45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	65	70	75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	95	100	105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	110	115	120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	140	145	150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	155	160	165	
Thr	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Thr	Gly	Arg	Ala	Ser	Cys	170	175	180	
Pro	Arg	Phe	Arg	Gln	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Ile	Cys	185	190	195	
Lys	Cys	His	Lys	Gly	Phe	Asp	Leu	Met	Tyr	Ile	Gly	Gly	Lys	Tyr	200	205	210	
Gln	Cys	His	Asp	Ile	Asp	Glu	Cys	Ser	Leu	Gly	Gln	Tyr	Gln	Cys	215	220	225	
Ser	Ser	Phe	Ala	Arg	Cys	Tyr	Asn	Val	Arg	Gly	Ser	Tyr	Lys	Cys	230	235	240	
Lys	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Asp	Gly	Leu	Thr	Cys	Val	Tyr	245	250	255	

Ile	Pro	Lys	Val	Met	Ile	Glu	Pro	Ser	Gly	Pro	Ile	His	Val	Pro	260	265	270
Lys	Gly	Asn	Gly	Thr	Ile	Leu	Lys	Gly	Asp	Thr	Gly	Asn	Asn	Asn	275	280	285
Trp	Ile	Pro	Asp	Val	Gly	Ser	Thr	Trp	Trp	Pro	Pro	Lys	Thr	Pro	290	295	300
Tyr	Ile	Pro	Pro	Ile	Ile	Thr	Asn	Arg	Pro	Thr	Ser	Lys	Pro	Thr	305	310	315
Thr	Arg	Pro	Thr	Pro	Lys	Pro	Thr	Pro	Ile	Pro	Thr	Pro	Pro	Pro	320	325	330
Pro	Pro	Pro	Leu	Pro	Thr	Glu	Leu	Arg	Thr	Pro	Leu	Pro	Pro	Thr	335	340	345
Thr	Pro	Glu	Arg	Pro	Thr	Thr	Gly	Leu	Thr	Thr	Ile	Ala	Pro	Ala	350	355	360
Ala	Ser	Thr	Pro	Pro	Gly	Gly	Ile	Thr	Val	Asp	Asn	Arg	Val	Gln	365	370	375
Thr	Asp	Pro	Gln	Lys	Pro	Arg	Gly	Asp	Val	Phe	Ser	Val	Leu	Val	380	385	390
His	Ser	Cys	Asn	Phe	Asp	His	Gly	Leu	Cys	Gly	Trp	Ile	Arg	Glu	395	400	405
Lys	Asp	Asn	Asp	Leu	His	Trp	Glu	Pro	Ile	Arg	Asp	Pro	Ala	Gly	410	415	420
Gly	Gln	Tyr	Leu	Thr	Val	Ser	Ala	Ala	Lys	Ala	Pro	Gly	Gly	Lys	425	430	435
Ala	Ala	Arg	Leu	Val	Leu	Pro	Leu	Gly	Arg	Leu	Met	His	Ser	Gly	440	445	450
Asp	Leu	Cys	Leu	Ser	Phe	Arg	His	Lys	Val	Thr	Gly	Leu	His	Ser	455	460	465
Gly	Thr	Leu	Gln	Val	Phe	Val	Arg	Lys	His	Gly	Ala	His	Gly	Ala	470	475	480
Ala	Leu	Trp	Gly	Arg	Asn	Gly	Gly	His	Gly	Trp	Arg	Gln	Thr	Gln	485	490	495
Ile	Thr	Leu	Arg	Gly	Ala	Asp	Ile	Lys	Ser	Glu	Ser	Gln	Arg		500	505	

<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 316

gatgggttcct gctcaagtcg cctg 24

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggaccacg tacg 24

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319

<211> 2110

<212> DNA

<213> Homo Sapien

<400> 319

cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50

tttagattgt gaaatgtggc tcaagggtctt cacaactttc ctttcctttg 100

caacagggtgc ttgctcgggg ctgaagggtga cagtgccatc acacactgtc 150

catggcgctca gaggtcaggc cctctaccta cccgtccact atggcttcca 200

cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250

caatgccccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300

ttggaatacc aacacaagtt caccatgatg ccaccaatg catctctgct 350

tatcaacca ctgcagttcc ctgatgaagg caattacatc gtgaagggtca 400

acattcaggg aatggaact ctatctgccca gtcagaagat acaagtcacg 450

gttgatgatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500

ggctgtggag tatgtgggga acatgaccct gacatgccat gtggaagggg 550

gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600
agctccacct actccttttc tccccaaaac aatacccttc atattgctcc 650
agtaaccaag gaagacattg ggaattacag ctgcctgggtg aggaaccctg 700
tcagtgaaat ggaaagtgat atcattatgc ccatcatata ttatggacct 750
tatggacttc aagtgaattc tgataaaggg ctaaaagtag gggaagtgtt 800
tactgttgac cttggagagg ccatcctatt tgattgttct gctgattctc 850
atcccccaa cacctactcc tggattagga ggactgacaa tactacatat 900
atcattaagc atgggcctcg cttagaagtt gcatctgaga aagtagcca 950
gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000
aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050
cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100
atcactatth ttgattatat ccatgtgtct tctcttctta tggaaaaaat 1150
atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200
gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250
cttcggaata tatgaatttg ttgcttttcc agatgtttct ggtgtttcca 1300
ggattccaag caggctctgtt ccagcctctg attgtgtatc ggggcaagat 1350
ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400
agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450
ttctgaagaa acattttaag gaaaaacagt ggaaaagtat attaactctgg 1500
aatcagtga gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550
tgcagaatag aggcattht gcaaattgaa ctgcaggtht ttcagcatat 1600
acacaatgtc ttgtgcaaca gaaaaacatg ttgggggaaat attcctcagt 1650
ggagagtcgt tctcatgctg acgggggagaa cgaaagtgac aggggtttcc 1700
tcataagtht tgtatgaaat atctctacaa acctcaatta gttctactct 1750
acactthcac tatcatcaac actgagacta tcctgtctca cctacaaatg 1800
tggaaactth acattgttcg atthtttcagc agactthgtt ttattaaatt 1850
thttattagt ttaagaatgc taaatttatg thtcaattth atttccaaat 1900
thctatcttg thattthgtac aacaaagtaa taaggatggt tgtcacaaaa 1950
acaaaactat gcctthctct thththtcaat caccagtagt atththtgaga 2000

agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050

tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttaaaa 2100

aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
1				5					10					15

Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser
				65					70					75

Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro
				80					85					90

Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu
				95					100					105

Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu
				110					115					120

Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr
				125					130					135

Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr
				140					145					150

Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg
				155					160					165

Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser
				170					175					180

Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala
				185					190					195

Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg
				200					205					210

Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile
				215					220					225

Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu
				230					235					240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu
				245					250					255
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp
				260					265					270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro
				275					280					285
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp
				290					295					300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu
				305					310					315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu
				320					325					330
Ala	Gln	Lys	Gly	Lys	Ser	Leu	Ser	Pro	Leu	Ala	Ser	Ile	Thr	Gly
				335					340					345
Ile	Ser	Leu	Phe	Leu	Ile	Ile	Ser	Met	Cys	Leu	Leu	Phe	Leu	Trp
				350					355					360
Lys	Lys	Tyr	Gln	Pro	Tyr	Lys	Val	Ile	Lys	Gln	Lys	Leu	Glu	Gly
				365					370					375
Arg	Pro	Glu	Thr	Glu	Tyr	Arg	Lys	Ala	Gln	Thr	Phe	Ser	Gly	His
				380					385					390
Glu	Asp	Ala	Leu	Asp	Asp	Phe	Gly	Ile	Tyr	Glu	Phe	Val	Ala	Phe
				395					400					405
Pro	Asp	Val	Ser	Gly	Val	Ser	Arg	Ile	Pro	Ser	Arg	Ser	Val	Pro
				410					415					420
Ala	Ser	Asp	Cys	Val	Ser	Gly	Gln	Asp	Leu	His	Ser	Thr	Val	Tyr
				425					430					435
Glu	Val	Ile	Gln	His	Ile	Pro	Ala	Gln	Gln	Gln	Asp	His	Pro	Glu
				440					445					450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50

cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgctg catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aattttatgc cccgtggtgc cctgcttgtc aaaatcttca 200

accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300

ataactgctc ttctactat ttatcattgt aaagatgggtg aatttaggcg 350

ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400

aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450

gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500

gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550

catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600

ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgcag 650

accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700

aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750
tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900
aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950
ttgcaggggt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000
acataaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050
gatggtttaa atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100
atztatgtat atttgtttta taataaccta tttcaagtct gagttttgaa 1150
aatttacatt tccaagtat tgcattattg aggtatttaa gaagattatt 1200
ttagagaaaa atatttctca tttgatataa tttttctctg tttcactgtg 1250
tgaaaaaaag aagatatttc ccataaatgg gaagtttgcc cattgtctca 1300
agaaatgtgt atttcagtga caatttcgtg gtcttttttag aggtatattc 1350
caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400
attaattaat tacagttttc tacacatggg aatacaggat atgctactga 1450
tttaggaagt ttttaagttc atgggtattct cttgattcca acaaagtttg 1500
attttctctt gtatttttct tacttactat gggttacatt ttttattttt 1550
caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600
tatttttttg ttgtttcaaa ctgaagttaa ctgagagatc catcaaattg 1650
aacaatctgt tgtaatttaa aattttggcc acttttttca gattttacat 1700
cattcttgct gaacttcaac ttgaaattgt ttttttttct tttttggatg 1750
tgaaggtgaa cattcctgat ttttgtctga tgtgaaaaag ccttggtatt 1800
ttacattttg aaaattcaaa gaagcttaat ataaaagtgt gcattctact 1850
caggaaaaag catcttcttg tatatgtctt aaatgtattt ttgtcctcat 1900
atacagaaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950
aaataataac atttttatat tttttaaaag acaaacttca tattatcctg 2000
tgttctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050
gtaggatgga acattttagt gtatttttac tccttaaaga gctagaatac 2100
atagttttca ccttaaaaga agggggaaaa tcataaatac aatgaatcaa 2150

ctgaccatta cgtagtagac aatttctgta atgtcccctt ctttctaggc 2200
tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tataacaagtt 2250
ttctttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300
tttgatgtg taacttgtga tgccttagaa aaatataccta agcacaaaat 2350
aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val	1	5	10	15
Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn	20	25	30	
Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly	35	40	45	
Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln	50	55	60	
Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp	65	70	75	
Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly	80	85	90	
Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His	95	100	105	
Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys	110	115	120	
Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile	125	130	135	
Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser	140	145	150	
Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys	155	160	165	
His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser	170	175	180	
Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu	185	190	195	

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu
215 220 225

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
260 265 270

Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgacaggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

<400> 331
gcgagtgtcc agctgcggag acccgtgata attcgttaac taattcaaca 50
aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100
ggacaggcgg attggaagag cggaaggctc ctggcccaga gcagtgtgac 150
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
ggtttgggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300
agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350
ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400
tacctggctc accctgtgaa tgcctacaaa ctgggtgaagc ggctaaacac 450
agactggcct gcgctggagg accttgctct gcaggactca gctgcagggt 500
ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550
gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600
ggaccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650
caatgctgag tgtggatgac tgctttggga tgggccgctc ggctacaat 700
gaaggggact attatcatac ggtgttgttg atggagcagg tgctaaagca 750
gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800
acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgcctggag 850

ctaccccgcc gcctgctctc ccttgacca agccacgaac gagctggagg 900
 gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950
 taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000
 aggcctgtgg actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050
 tggggagggt gtcaaactga caccctgtag acagaagagg cttttctgta 1100
 ggtaccacca tggcaacagg gcccacagc tgctcattgc ccccttcaaa 1150
 gaggaggacg agtgggacag cccgcacatc gtcaggtagt acgatgtcat 1200
 gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250
 cacgagccac cgttcgtgat cccaagacag gagtccctac tgtcgccagc 1300
 taccgggttt ccaaaagctc ctggctagag gaagatgatg accctgttgt 1350
 ggcccgagta aatcgctcga tgcagcatat cacagggtta acagtaaaga 1400
 ctgcagaatt gttacagggt gcaaattatg gagtgggagg acagtatgaa 1450
 ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaacaga 1500
 ggggaatagg ttagcgacgt ttcttaacta catgagtgat gtagaagctg 1550
 gtggtgccac cgtcttccct gatctggggg ctgcaatttg gcctaagaag 1600
 ggtacagctg tgttctggta caacctcttg cggagcgggg aaggtgacta 1650
 ccgaacaaga catgctgcct gccctgtgct tgtgggctgc aagtgggtct 1700
 ccaataagtg gttccatgaa cgaggacagg agttcttgag accttggtga 1750
 tcaacagaag ttgactgaca tccttttctg tccttccct tcctggctct 1800
 tcagcccatg tcaacgtgac agacaccttt gtatgttcct ttgtatgttc 1850
 ctatcaggct gatTTTTTga gaaatgaatg tttgtctgga gcagaggagg 1900
 accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950
 gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000
 gttagctgtc tagcgcttag caagggtcct ttgtacctca ggtgttttag 2050
 gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100
 gtttttatgg catttctatc tattgtggct ttacaaaaa ataaaatgtc 2150
 cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val
1				5					10					15
Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
				20					25					30
Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35					40					45
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50					55					60
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65					70					75
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80					85					90
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95					100					105
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110					115					120
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125					130					135
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140					145					150
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155					160					165
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170					175					180
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185					190					195
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu
				200					205					210
Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg
				215					220					225
Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His
				230					235					240
Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu
				245					250					255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu
				260					265					270

Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480
Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr	485	490	495
Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp	500	505	510
Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg	515	520	525
Pro Cys Gly Ser Thr Glu Val Asp	530		

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336

acactcagca ttgcctggta cttg 24

<210> 337

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 337

gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

gcagtattga gttttacttc ctctcttttt tagtggaaga cagaccataa 50
tcccagtggtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100
ggtagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150
agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200
gctctgtctt tggcctcatt gaccccaggt tctctgggta aaactgaaag 250
cctactactg gcctgggtgcc catcaatcca ttgatccttg aggctgtgcc 300
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350
ttggctctgc tgcggccagc gcttccctc atcttagggc tgtctctggg 400
gtgcagcctg agcctcctgc gggtttctctg gatccagggg gagggagaag 450
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550
cccctactac agggacccca acaagcccta caagaagggtg ctcaggactc 600
ggtacatcca gacagagctg ggctccctg agcgggtgct ggtggctgtc 650
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700
ggtggeccat cacttccctc gggtactcta cttactggg cagcgggggg 750
cccgggctcc agcagggatg cagggtgggtg ctcattgggga tgagcggccc 800
gcctggctca tgtcagagac cctgcgccac cttcacacac actttggggc 850
cgactacgac tggttcttca tcatgcagga tgacacatat gtgcaggccc 900
cccgcctggc agcccttgct ggccacctca gcatcaacca agacctgtac 950
ttaggccggg cagaggagtt cattggcgca ggcgagcagg cccggtactg 1000
tcattgggggc tttggctacc tgttgtcacg gagtctctg cttcgtctgc 1050
ggccacatct ggatggctgc cgaggagaca ttctcagtgc ccgtcctgac 1100
gagtggcttg gacgctgcct cattgactct ctgggcgtcg gctgtgtctc 1150
acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200
accctgagaa ggaagggagc tcggctttcc tgagtgcctt cgccgtgcac 1250
cctgtctccg aaggtaccct catgtaccgg ctccacaaac gcttcagcgc 1300
tctggagttg gagcgggctt acagtgaaat agaacaactg caggctcaga 1350
tccggaacct gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400

cccggttgggc tccctgctcc ttccacacca cactctcgct ttgaggtgct 1450
gggctgggac tacttcacag agcagcacac cttctcctgt gcagatgggg 1500
ctcccaagtg ccactacag ggggctagca gggcggacgt gggatgatgcg 1550
ttggagactg ccctggagca gctcaatcgg cgctatcagc cccgcctgcg 1600
cttcagaag cagcgactgc tcaacggcta tcggcgcttc gaccagcac 1650
ggggcatgga gtacaccctg gacctgctgt tggaatgtgt gacacagcgt 1700
gggcaccggc gggccctggc tcgcagggtc agcctgctgc ggccactgag 1750
ccgggtggaa atcctaccta tgccctatgt cactgaggcc acccgagtgc 1800
agctggtgct gccactcctg gtggctgaag ctgctgcagc cccggctttc 1850
ctcgaggcgt ttgcagcaa tgtcctggag ccacgagaac atgcattgct 1900
caccctgttg ctggtctacg ggccacgaga aggtggccgt ggagctccag 1950
accattttct tggggtgaag gctgcagcag cggagttaga gcgacggtag 2000
cctgggacga ggctggcctg gctcgctgtg cgagcagagg ccccttccca 2050
ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100
tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150
tgtcgcatga atgccatctc tggctggcag gccttctttc cagtccattt 2200
ccaggagttc aatcctgccc tgtcaccaca gagatcacc ccaggggccc 2250
cgggggctgg ccctgacccc ccctcccctc ctggtgctga cccctcccgg 2300
ggggctccta taggggggag atttgaccgg caggcttctg cggagggtg 2350
cttctacaac gctgactacc tggcggcccg agcccggtg gcagggtgaac 2400
tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450
gttttctctc gggtctcagg gctccacctc tttcgggccg tagagccagg 2500
gctggtgcag aagttctccc tgcgagactg cagcccacgg ctcatggaag 2550
aactctacca ccgctgccg ctcagcaacc tggaggggct agggggccgt 2600
gccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650
gcccgcctgg gggccctaac ctcatcactc ttcctttgtc tgcctcagcc 2700
ccaggaaggg caaggcaaga tgggtggacag atagagaatt gttgctgtat 2750
tttttaaata tgaaaatgtt attaaacatg tcttctgcc 2789

<210> 339
 <211> 772
 <212> PRT
 <213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro	1	5	10	15
Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg	20	25	30	
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala	35	40	45	
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg	50	55	60	
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr	65	70	75	
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg	80	85	90	
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala	95	100	105	
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val	110	115	120	
Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr	125	130	135	
Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser	140	145	150	
His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg	155	160	165	
His	Leu	His	Thr	His	Phe	Gly	Ala	Asp	Tyr	Asp	Trp	Phe	Phe	Ile	170	175	180	
Met	Gln	Asp	Asp	Thr	Tyr	Val	Gln	Ala	Pro	Arg	Leu	Ala	Ala	Leu	185	190	195	
Ala	Gly	His	Leu	Ser	Ile	Asn	Gln	Asp	Leu	Tyr	Leu	Gly	Arg	Ala	200	205	210	
Glu	Glu	Phe	Ile	Gly	Ala	Gly	Glu	Gln	Ala	Arg	Tyr	Cys	His	Gly	215	220	225	
Gly	Phe	Gly	Tyr	Leu	Leu	Ser	Arg	Ser	Leu	Leu	Leu	Arg	Leu	Arg	230	235	240	
Pro	His	Leu	Asp	Gly	Cys	Arg	Gly	Asp	Ile	Leu	Ser	Ala	Arg	Pro	245	250	255	

Asp	Glu	Trp	Leu	Gly	Arg	Cys	Leu	Ile	Asp	Ser	Leu	Gly	Val	Gly	
				260					265					270	
Cys	Val	Ser	Gln	His	Gln	Gly	Gln	Gln	Tyr	Arg	Ser	Phe	Glu	Leu	
				275					280					285	
Ala	Lys	Asn	Arg	Asp	Pro	Glu	Lys	Glu	Gly	Ser	Ser	Ala	Phe	Leu	
				290					295					300	
Ser	Ala	Phe	Ala	Val	His	Pro	Val	Ser	Glu	Gly	Thr	Leu	Met	Tyr	
				305					310					315	
Arg	Leu	His	Lys	Arg	Phe	Ser	Ala	Leu	Glu	Leu	Glu	Arg	Ala	Tyr	
				320					325					330	
Ser	Glu	Ile	Glu	Gln	Leu	Gln	Ala	Gln	Ile	Arg	Asn	Leu	Thr	Val	
				335					340					345	
Leu	Thr	Pro	Glu	Gly	Glu	Ala	Gly	Leu	Ser	Trp	Pro	Val	Gly	Leu	
				350					355					360	
Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	
				365					370					375	
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	
				380					385					390	
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	
				395					400					405	
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	
				410					415					420	
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	
				425					430					435	
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	
				440					445					450	
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	
				455					460					465	
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	
				470					475					480	
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	
				485					490					495	
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	
				500					505					510	
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	
				515					520					525	
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	
				530					535					540	

Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	
				545						550				555	
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	
				560					565					570	
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	
				575					580					585	
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	
				590					595					600	
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	
				605					610					615	
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	
				620					625					630	
Ser	Pro	Gln	Arg	Ser	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Gly	Pro	Asp	
				635					640					645	
Pro	Pro	Ser	Pro	Pro	Gly	Ala	Asp	Pro	Ser	Arg	Gly	Ala	Pro	Ile	
				650					655					660	
Gly	Gly	Arg	Phe	Asp	Arg	Gln	Ala	Ser	Ala	Glu	Gly	Cys	Phe	Tyr	
				665					670					675	
Asn	Ala	Asp	Tyr	Leu	Ala	Ala	Arg	Ala	Arg	Leu	Ala	Gly	Glu	Leu	
				680					685					690	
Ala	Gly	Gln	Glu	Glu	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Glu	Val	Met	
				695					700					705	
Asp	Val	Phe	Leu	Arg	Phe	Ser	Gly	Leu	His	Leu	Phe	Arg	Ala	Val	
				710					715					720	
Glu	Pro	Gly	Leu	Val	Gln	Lys	Phe	Ser	Leu	Arg	Asp	Cys	Ser	Pro	
				725					730					735	
Arg	Leu	Ser	Glu	Glu	Leu	Tyr	His	Arg	Cys	Arg	Leu	Ser	Asn	Leu	
				740					745					750	
Glu	Gly	Leu	Gly	Gly	Arg	Ala	Gln	Leu	Ala	Met	Ala	Leu	Phe	Glu	
				755					760					765	
Gln	Glu	Gln	Ala	Asn	Ser	Thr									
				770											

<210> 340
 <211> 1572
 <212> DNA
 <213> Homo Sapien

<400> 340
 cggagtgggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50
 tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100

ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
accaaact gtgacaaagc agagtctctc agttctgaaa atgttaaagt 400
gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450
aagcttacia atacgccttt gataagtata gagaccaata caactgggtc 500
ttccttgac gccccactac gtttgctatc attgaaaacc taaagtattt 550
tttgtaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600
aatctggaga ctttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750
cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800
gatggaaaag atgtatttaa taccaaactc gttgggcttt ctattaaaga 850
ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900
tggctgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950
tatgggggat accgccttag ggcatttggg catattttca atgatgcatt 1000
ggttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050
agcgtgaata tgatctttgt ataggacgtg tgttgtcatt atttgtagta 1100
gtaactacat atccaatata gctgtatgtt tctttttctt ttctaatttg 1150
gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaata 1200
gggtgggttt tttctttaaa acacatgaac attgtaaatg tgttggaag 1250
aagtgtttta agaataataa ttttgcaa ataaactattaa taaatattat 1300
atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350
tttgctgatt ggttaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400
gcaaatgata tctctagttg tgaatttgtg attaaagtaa aacttttagc 1450
tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctcccaa 1500

gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550

attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

<400> 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly
1				5					10					15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
				20					25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
				35					40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
				50					55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
				65					70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
				80					85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
				95					100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
				110					115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
				125					130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
				140					145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
				155					160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
				170					175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
				185					190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
				200					205					210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
				215					220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
				230					235					240

Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
				245					250					255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys
				260					265					270
Cys	Ser	Asp	Met	Ala	Val	Thr	Phe	Asn	Gly	Leu	Thr	Pro	Asn	Gln
				275					280					285
Met	His	Val	Met	Met	Tyr	Gly	Val	Tyr	Arg	Leu	Arg	Ala	Phe	Gly
				290					295					300
His	Ile	Phe	Asn	Asp	Ala	Leu	Val	Phe	Leu	Pro	Pro	Asn	Gly	Ser
				305					310					315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 345
gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 346
gggatgcagg tgggtgtctca tgggg 25

<210> 347
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 347
ccctcatgta cgggctcc 18

<210> 348
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 348
ggattctaatac gactcact atagggctca gaaaagcgca acagagaa 48

<210> 349
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 349
ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 350
ggattcta acgactcact atagggcggc gatgtccact ggggctac 48

<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 351
ctatgaaatt aaccctcact aaaggacga ggaagatggg cggatggt 48

<210> 352
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 352
ggattcta acgactcact atagggcacc cacgcgtccg gctgctt 47

<210> 353
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 353
ctatgaaatt aaccctcact aaaggacgg gggacaccac ggaccaga 48

<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 354
ggattcta acgactcact atagggcttg ctgcggtttt tgttcctg 48

<210> 355
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 355

ctatgaaatt aaccctcact aaaggagct gccgatcca ctggtatt 48

<210> 356

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 356

ggattctaatt acgactcact atagggcgga tcctggcgg cctctg 46

<210> 357

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 357

ctatgaaatt aaccctcact aaaggagcc cgggcatggt ctcagtta 48

<210> 358

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 358

ggattctaatt acgactcact atagggcggg aagatggcga ggaggag 47

<210> 359

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 359

ctatgaaatt aaccctcact aaaggacca aggccacaaa cggaaatc 48

<210> 360

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 360

ggattctaatt acgactcact atagggctgt gctttcattc tgccagta 48

<210> 361
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 361
ctatgaaatt aaccctcact aaagggaggg tacaattaag gggtaggat 48

<210> 362
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 362
ggattctaatt acgactcact atagggcccg cctcgctcct gctcctg 47

<210> 363
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 363
ctatgaaatt aaccctcact aaagggagga ttgccgagac cctcacag 48

<210> 364
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 364
ggattctaatt acgactcact atagggcccc tctgccttc cctgtcc 47

<210> 365
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 365
ctatgaaatt aaccctcact aaagggagtg gtggccgcga ttatctgc 48

<210> 366
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 366
ggattctaatacgcactcactatagggcgcgatggcagcgatgagg48

<210> 367
<211> 47

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 367
ctatgaaattaacccctcactaaagggacagacggggcagagggagtgg47

<210> 368
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 368
ggattctaatacgcactcactatagggccaggaggcgtgaggagaaac47

<210> 369
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 369
ctatgaaattaacccctcactaaagggaaagacatgtcatcgggagtgg48

<210> 370
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 370
ggattctaatacgcactcactatagggccgggtggaggtggaacagaaa48

<210> 371
<211> 48
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatacgcactcactatagggccaggaaatccggatgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggattctaatacgcactcactatagggccagctacccgcaggaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaagag 50
agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100
aaaaaatgaa ttcattctaaa tcattctgaaa cacaatgcac agagagagga 150
tgcttctctt cccaaatggt cttatggact gttgctggga tccccatcct 200
atttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcatct 250
ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300
ctctcctgct acaattatgg atcagggttca gtcaagaatt gttgtccatt 350
gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400
tttcctgggc gttaagttaa aagaactgct cagccatggg ggctcacctg 450
gtgggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500
taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgaggggtc 550
agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600
gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650
gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700
tcaattatth tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750
ggaaaatctc tttaagaaca gaaggcacia ctcaaattgt taaagaagga 800
agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgctc 850
tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900
taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly
1				5					10					15
Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro
				20					25					30
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
				35					40					45
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro

50										55					60				
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser					
				65					70					75					
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser					
				80					85					90					
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu					
				95					100					105					
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser					
				110					115					120					
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg					
				125					130					135					
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp					
				140					145					150					
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp					
				155					160					165					
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala					
				170					175					180					
Thr	Met	Arg	Asp	Ser	Ser	Asn	Pro	Arg	Gln	Asn	Trp	Asn	Asp	Val					
				185					190					195					
Thr	Cys	Phe	Leu	Asn	Tyr	Phe	Arg	Ile	Cys	Glu	Met	Val	Gly	Ile					
				200					205					210					
Asn	Pro	Leu	Asn	Lys	Gly	Lys	Ser	Leu											
				215															

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 380
ggaggactgt gccacatga gagactcttc aaaccaagg caaaattgg 49

<210> 381
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
gcagattttg aggacagcca cctcca 26

<210> 382
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
ggccttgag acaaccgt 18

<210> 383
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
cagactgagg gagatccgag a 21

<210> 384
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 384
cagctgccct tccccaacca 20

<210> 385
<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 385
catcaagcgc ctctacca 18

<210> 386
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386
cacaaactcg aactgcttct g 21

<210> 387
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 387
gggcatcac agctccct 18

<210> 388
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 388
gggatgtggt gaacacagaa ca 22

<210> 389
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 389
tgccagctgc atgctgccag tt 22

<210> 390
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcagggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 395
ccgcagcctc agtgatga 18

<210> 396
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 396
gaagagcaca gctgcagatc c 21

<210> 397
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 397
gaggtgtcct ggctttggta gt 22

<210> 398
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 398
cctctggcgc cccactcaa 20

<210> 399
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 399
ccaggagagc tggcgatg 18

<210> 400
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 400
gcaaattcag ggctcactag aga 23

<210> 401
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 401
cacagagcat ttgtccatca gcagttcag 29

<210> 402
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 402
ggcagagact tccagtcact ga 22

<210> 403
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 403
gccaaaggtg gtgtagata gg 22

<210> 404
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
caggccccct tgatctgtac ccca 24

<210> 405
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 405

gggacgtgct tctacaagaa cag 23

<210> 406
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
caggcttaca atgttatgat cagaca 26

<210> 407
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 407
tattcagagt tttccattgg cagtgccagt t 31

<210> 408
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 408
tctacatcag cctctctgcg c 21

<210> 409
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 409
cgatcttctc cacccaggag cgg 23

<210> 410
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 410
gccaggcctc acattcgt 18

<210> 411
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
ctccctgaat ggcagcctga gca 23

<210> 412
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
aggtgtttat taagggccta cgct 24

<210> 413
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cagagcagag ggtgccttg 19

<210> 414
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 414
tggcggagtc ccctcttggc t 21

<210> 415
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 415
ccctgtttcc ctatgcatca ct 22

<210> 416

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
tcaaccctg accctttcct a 21

<210> 417
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
ggcaggggac aagccatctc tcct 24

<210> 418
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
gggactgaac tgccagcttc 20

<210> 419
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 419
gggccctaac ctcattacct tt 22

<210> 420
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 420
tgtctgcctc agccccagga agg 23

<210> 421
<211> 21
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

tctgtccacc atcttgccctt g 21

<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

<400> 422

gggactacaa gccgcgccgc gctgccgctg gcccctcagc aaccctcgac 50
atggcgctga ggcgccacc gcgactccgg ctctgcgctc ggctgcctga 100
cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150
tcaaatccag caatcgaacc ccagtgggtac aggaatttga aagtgtggaa 200
ctgtcttgca tcattacgga ttgcgagaca agtgacccca ggatcgagtg 250
gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
ttcagggaga cttggcggtt cgtgcagaaa tactggggaa gacatccctg 350
aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400
cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450
ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500
ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550
ccggcctcac tacagctggt atcgcaatga tgtaccactg cccacggatt 600
ccagagccaa tcccagattt cgcaattctt ctttcactt aaactctgaa 650
acaggcactt tgggtgttcac tgctgttcac aaggacgact ctgggcagta 700
ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750
agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800
gttgtccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850
cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900
accagggaa accagatgga gttaactaca tccgcactga cgaggagggc 950
gacttcagac acaagtcacg gtttgtgatc tgagaccgc ggtgtggctg 1000
agagcgcaca gagcgcacgt gcacatacct ctgctagaaa ctctgtcaa 1050
ggcagcgaga gctgatgcac tcggacagag ctagacactc attcagaagc 1100

ttttcgtttt ggccaaagtt gaccactact cttcttactc taacaagcca 1150
catgaataga agaattttcc tcaagatgga cccggtaaata ataaccacaa 1200
ggaagcgaaa ctgggtgcgt tctactgagtt gggttcctaa tctgtttctg 1250
gcctgattcc cgcatgagta ttaggggtgat cttaaagagt ttgctcacgt 1300
aaacgcccgt gctggggccct gtgaagccag catgttcacc actggtcggt 1350
cagcagccac gacagcacca tgtgagatgg cgagggtggct ggacagcacc 1400
agcagcgcat cccggcgagg acccagaaaa ggcttcttac acagcagcct 1450
tacttcatcg gccacagac accaccgcag tttcttctta aaggctctgc 1500
tgatcgggtgt tgcagtgctc attgtggaga agcttttttg atcagcattt 1550
tgtaaaaaca accaaaatca ggaaggtaaa ttggttgctg gaagagggat 1600
cttgccctgag gaaccctgct tgtccaacag ggtgtcagga tttaaggaaa 1650
accttcgtct taggctaagt ctgaaatggg actgaaatat gcttttctat 1700
gggtcttggt tattttataa aattttacat cttaaatttt gctaaggatg 1750
tattttgatt attgaaaaga aaatttctat ttaaactgta aatatattgt 1800
catacaatgt taaataacct atttttttta aaaagttcaa cttaggtag 1850
aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900
ttttaccaa ggaatcctct catggaagtt tactgtgatg ttctttttct 1950
cacacaagtt ttagcctttt tcacaaggga actcactactg tctacacatc 2000
agaccatagt tgcttaggaa accttttaaaa attccagtta agcaatgttg 2050
aaatcagttt gcatctcttc aaaagaaacc tctcagggtta gctttgaact 2100
gcctcttctt gagatgacta ggacagtctg taccagagg ccaccagaa 2150
gccctcagat gtacatacac agatgccagt cagctcctgg ggttgcgcca 2200
ggcgcccccg ctctagctca ctgttgcttc gctgtctgcc aggaggccct 2250
gccatccttg ggccctggca gtggctgtgt ccagtgagc ttactcacg 2300
tggcccttgc ttcattccagc acagctctca ggtgggcact gcaggacac 2350
tggtgtcttc catgtagcgt ccagctttg ggctcctgta acagacctct 2400
ttttggttat ggatggctca caaaataggg cccccaatgc tatttttttt 2450
ttttaagttt gttaattat ttgttaagat tgtctaaggc caaaggcaat 2500

tgcgaaatca agtctgtcaa gtacaataac attttttaaaa gaaaatggat 2550
 cccactgttc ctcttttgcca cagagaaagc acccagacgc cacaggctct 2600
 gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650
 aaagaacgtc aggtggagca gccagggtgaa aggcctggcg gggaggaaag 2700
 tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750
 atccgccgga gacactgttc ccatttgtgg ggggacatta gcaacatcac 2800
 tcagaagcct gtgtttttca agagcagggtg ttctcagcct cacatgccct 2850
 gccgtgctgg actcaggact gaagtgtgtg aaagcaagga gctgctgaga 2900
 aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcaccttgt 2950
 ctttcagctt ccagtgtctt gggtttttta tactttgaca gctttttttt 3000
 aattgcatat atgagactgt gttgactttt tttagttatg tgaaacactt 3050
 tgccgcaggc cgctggcag aggcaggaaa tgctccagca gtggctcagt 3100
 gctccctggt gtctgtgca tggcatcctg gatgcttagc atgcaagttc 3150
 cctccatcat tgccaccttg gtagagaggg atggctcccc accctcagcg 3200
 ttggggattc acgctccagc ctccttcttg gttgtcatag tgatagggta 3250
 gccttattgc cccctcttct tataccctaa aaccttctac actagtgcc 3300
 tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350
 gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatttt 3400
 aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450
 gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500
 caccgtaatt tggcatttgt ttaacctcat ttataaaagc ttcaaaaaaa 3550
 ccca 3554

<210> 423

<211> 310

<212> PRT

<213> Homo Sapien

<400> 423

Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu
1					5			10						15
Pro	Asp	Phe	Phe	Leu	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly
				20				25						30
Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu





Creation date: 10-29-2003
Indexing Officer: HNGUYEN13 - HIEU NGUYEN
Team: OIPEBackFileIndexing
Dossier: 09904766

Legal Date: 02-15-2002

No.	Doccode	Number of pages
1	CRFL	6

Total number of pages: 6

Remarks:

Order of re-scan issued on